5_3_Magic_BLAST_contigs_specific

July 31, 2021

Summary of magicblast

[1]:
```
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns
from pandas.plotting import scatter_matrix
import pathlib
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```
from IPython.core.display import display, HTML
display(HTML("<style>.container { width:95% !important; }</style>"))
```

```
<IPython.core.display.HTML object>
```

[3]:
```
PROJECT_CODE='PRJNA573298'
BASE_PATH = f'/mnt/1TB_0/Data/Assembly/{PROJECT_CODE}/'

dbname='nt'
kmer='k141'

#magicblast on contigs
magic_blast_sam_tail=f'_{dbname}_final_contigs_magicBLAST.sam'
f_contigs_file_tail=f'_{dbname}_magic_blast_asc_contigs.txt'
GIS,ACCESSIONS,TITLES=None,None,None
```

0.0.1 All SRA's

[4]:
```
sra_list=['SRR10168373','SRR10168374',\
      'SRR10168375','SRR10168376',\
      'SRR10168377','SRR10168378',\
      'SRR10168379','SRR10168380',\
      'SRR10168381','SRR10168382',\
      'SRR10168383','SRR10168384',\
      'SRR10168385','SRR10168386',\
      'SRR10168387','SRR10168388',\
      'SRR10168389','SRR10168390',\
```

```
    'SRR10168391','SRR10168392','SRR10168393']
```

[5]:
```
def read_gi_accession_title(gi_asc_file):
    gis=[]
    accessions=[]
    titles=[]
    with open(gi_asc_file, 'r') as infile:
        data = infile.readlines()
        for i in data:
            output=i.split(' ',2)
            gis.append(output[0])
            accessions.append(output[1])
            titles.append(output[2])
    return gis, accessions, titles
```

[6]:
```
def set_accessions():
    global GIS
    global ACCESSIONS
    global TITLES
    GIS,ACCESSIONS,TITLES=read_gi_accession_title('/mnt/1TB_ssd/Data/BLAST/nt.
↪gi_taxid.tsv')
```

0.0.2 Stats

[7]:
```
def get_asc_descr_count(sra):
    accessions=[]
    descriptions=[]
    counts=[]
    path = BASE_PATH+sra+'/magic_blast/'
    with open(path+f'{sra}_{dbname}_{kmer}_magicBLAST_summary.txt', 'r') as f:
        lines = [line.rstrip('\n') for line in f]
        total=len(lines)-1
        for line in lines:
            if not 'database:' in line: #ignore header
                asc=line.split(None, 1)[0]
                title=line.split(None, 1)[1].split(', count:')[0]
                count=line.split(None, 1)[1].split(', count:')[1]
                accessions.append(asc)
                descriptions.append(title)
                counts.append(int(count))
    return accessions, descriptions, counts, total
```

[8]:
```
def get_indexes(substr, str_list):
    index_list = []
    i = 0
    for e in str_list:
        if substr in e.lower():
```

```
            index_list.append(i)
        i +=1
    return index_list
```

[9]:
```
for i,sra in enumerate(sra_list):
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    print(f'{sra}, matched contigs: {sum(counts)}')
    #for d,c in zip(descriptions, counts):
    #    print(f'{d}: {c}')
    #print('\n')
```

```
SRR10168373, matched contigs: 4348
SRR10168374, matched contigs: 4669
SRR10168375, matched contigs: 43799
SRR10168376, matched contigs: 23385
SRR10168377, matched contigs: 19599
SRR10168378, matched contigs: 14969
SRR10168379, matched contigs: 45840
SRR10168380, matched contigs: 33249
SRR10168381, matched contigs: 18395
SRR10168382, matched contigs: 3050
SRR10168383, matched contigs: 4954
SRR10168384, matched contigs: 15128
SRR10168385, matched contigs: 4704
SRR10168386, matched contigs: 2146
SRR10168387, matched contigs: 9448
SRR10168388, matched contigs: 4383
SRR10168389, matched contigs: 4398
SRR10168390, matched contigs: 8835
SRR10168391, matched contigs: 18251
SRR10168392, matched contigs: 35405
SRR10168393, matched contigs: 18335
```

[10]:
```
def get_desc_count(qstring, descriptions, counts, lowercase=True):
    qd=[]
    qc=0
    for d,c in zip(descriptions, counts):
        if lowercase:
            if qstring.lower() in d.lower():
                qd.append(d)
                qc=qc+int(c)
        else:
            if qstring in d:
                qd.append(d)
                qc=qc+int(c)
    #print(f'qstring: {qstring}, descriptions: {len(descriptions)}, qd: {qd},␣
 ↪counts: {len(counts)}, qc: {qc}')
```

```
    return qd, qc
```

[11]:
```
def get_desc_count_without(qstring, nqstring, descriptions, counts,␣
↪lowercase=True):
    qd=[]
    qc=0
    for d,c in zip(descriptions, counts):
        if lowercase:
            if qstring.lower() in d.lower() and nqstring.lower() not in d.
↪lower():
                qd.append(d)
                qc=qc+int(c)
        else:
            if qstring in d:
                qd.append(d)
                qc=qc+int(c)
    #print(f'qstring: {qstring}, descriptions: {len(descriptions)}, qd: {qd},␣
↪counts: {len(counts)}, qc: {qc}')
    return qd, qc
```

[12]:
```
def get_descr(sra):
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    #print(f'sra: {sra}, accessions: {len(accessions)}, descriptions:␣
↪{len(descriptions)}, counts: {len(counts)}, total: {total}')
    if total>0:
        human,humanc = get_desc_count('human', descriptions, counts)
        homo_sapiens,homo_sapiensc = get_desc_count('homo sapiens',␣
↪descriptions, counts)
        h_sapiens,h_sapiensc = get_desc_count('h.sapiens', descriptions, counts)
        human_contigs = human+homo_sapiens+h_sapiens
        human_counts = humanc+homo_sapiensc+h_sapiensc
        pangolin, pangolinc = get_desc_count('manis javanica', descriptions,␣
↪counts)
        pangolin_p, pangolin_pc = get_desc_count('manis pentadactyla',␣
↪descriptions, counts)
        pangolin=pangolin+pangolin_p
        pangolin_counts=pangolinc+pangolin_pc
        mouse,mousec = get_desc_count('mus musculus', descriptions, counts)
        vector,vectorc= get_desc_count('vector', descriptions, counts)
        pig,pigc = get_desc_count('sus scrofa', descriptions, counts)
        cat,catc = get_desc_count('felis catus', descriptions, counts)
        tiger,tigerc = get_desc_count('panthera tigris', descriptions, counts)
        dog,dogc = get_desc_count('canis lupus', descriptions, counts)
        virus,virusc = get_desc_count_without('virus', 'retrovirus',␣
↪descriptions, counts)
```

```
        mulatta,mulattac = get_desc_count('mulatta', descriptions, counts)
        troglodytes,troglodytesc = get_desc_count('troglodytes', descriptions,␣
↪counts)
        pongo,pongoc =get_desc_count('pongo', descriptions, counts)
        papio,papioc = get_desc_count('papio', descriptions, counts)
        mandrillus,mandrillusc =get_desc_count('mandrillus', descriptions,␣
↪counts)
        cercocebus,cercocebusc =get_desc_count('cercocebus', descriptions,␣
↪counts)
        gelada,geladac =get_desc_count('gelada', descriptions, counts)
        monkey = mulatta+troglodytes+pongo+papio+mandrillus+cercocebus+gelada
        monkey_counts =␣
↪mulattac+troglodytesc+pongoc+papioc+mandrillusc+cercocebusc+geladac

        mustela,mustelac= get_desc_count('mustela', descriptions, counts)

        pipistrellus,pipistrellusc =get_desc_count('pipistrellus',␣
↪descriptions, counts)
        rhinolophus,rhinolophusc = get_desc_count('rhinolophus', descriptions,␣
↪counts)
        pteropus,pteropusc = get_desc_count('pteropus', descriptions, counts)
        myotis,myotisc = get_desc_count('myotis', descriptions, counts)
        bat = pipistrellus + rhinolophus+pteropus+myotis
        bat_counts = pipistrellusc + rhinolophusc+pteropusc+myotisc

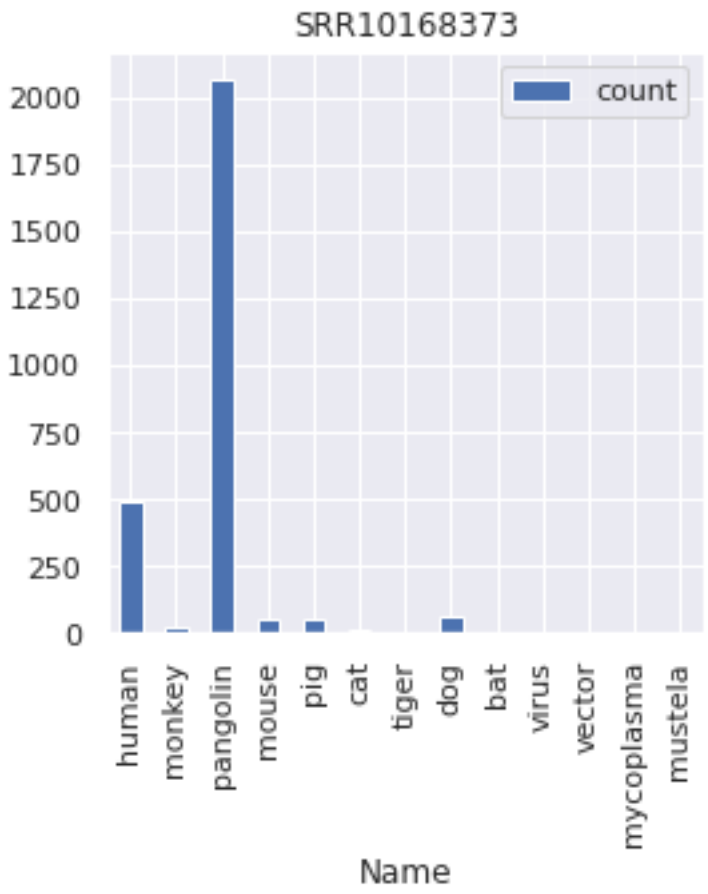
        mycoplasma,mycoplasmac = get_desc_count('mycoplasma', descriptions,␣
↪counts)

        lst = ['human', 'monkey', 'pangolin', 'mouse',
                'pig', 'cat', 'tiger', 'dog', 'bat', 'virus',␣
↪'vector','mycoplasma','mustela']
        lengths = [human_counts, monkey_counts, pangolin_counts, mousec,
                pigc, catc, tigerc, dogc, bat_counts, virusc, vectorc,␣
↪mycoplasmac,mustelac]
        final_contigs=BASE_PATH+sra+'/megahit_default/final.contigs.fa'
        with open(final_contigs) as final_contigs_file:
            total_contigs=sum(1 for _ in final_contigs_file)
        res = [int(i) for i in counts]
        total_contigs_matched=sum(res)
        sra_l=[sra]*len(lst)
        fractions_matched = [human_counts/total_contigs_matched, monkey_counts/
↪total_contigs_matched, pangolin_counts/total_contigs_matched, mousec/
↪total_contigs_matched,
```

```
                pigc/total_contigs_matched, catc/total_contigs_matched, tigerc/
↪total_contigs_matched, dogc/total_contigs_matched, bat_counts/
↪total_contigs_matched,
                             virusc/total_contigs_matched, vectorc/
↪total_contigs_matched, mycoplasmac/total_contigs_matched, mustelac/
↪total_contigs_matched]
        pct_matched = [round(i * 100,2) for i in fractions_matched]
        df = pd.DataFrame(list(zip(sra_l, lst, lengths, pct_matched)),
                    columns =['SRA','Name', 'count', 'pct_matched'])
        return df
    return None
```

[13]:
```
sns.set(rc={"figure.figsize":(4, 4)})
def plot_df(df, sra):
    ax=df.plot(x='Name', y='count', kind='bar')
    ax.set_title(sra, fontsize=12)
    #ax.set_yscale('log')
    #ax.set_ylim([0,df['count'].max()+10])
    ax.set_ylim(bottom=0)
    fig = plt.gcf()
    fig.savefig(BASE_PATH+sra+'/magic_blast/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species.png', bbox_inches="tight")
```

[14]:
```
for sra in sra_list:
    try:
        df=get_descr(sra)
        df.to_csv(BASE_PATH+sra+'/magic_blast/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species_df.csv')
        plot_df(df, sra)
    except FileNotFoundError:
        pass
    except AttributeError:
        pass
```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count
2000
1750
1500
1250
1000
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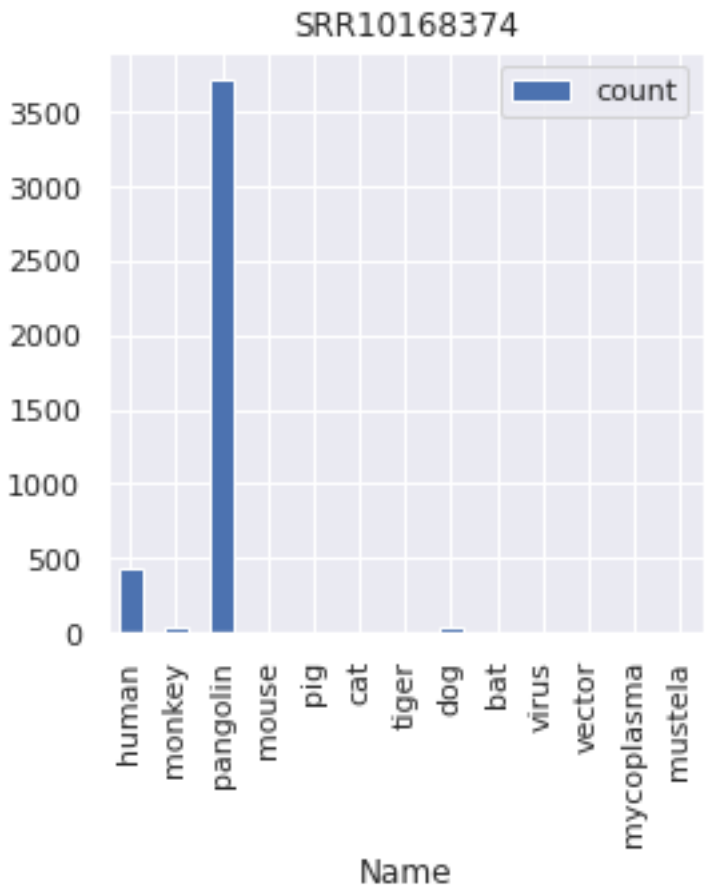
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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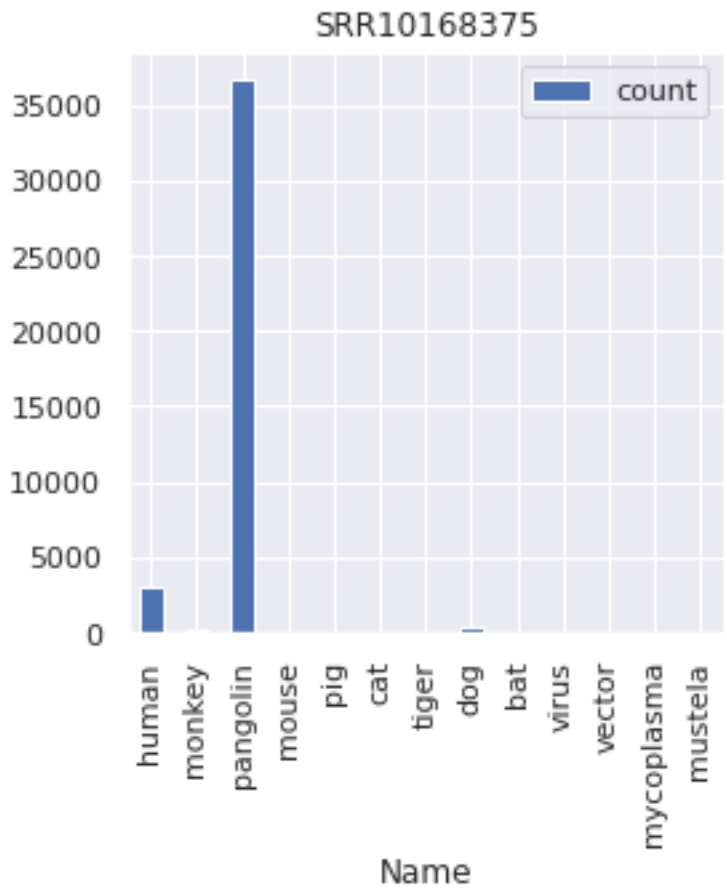
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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30000
25000
20000
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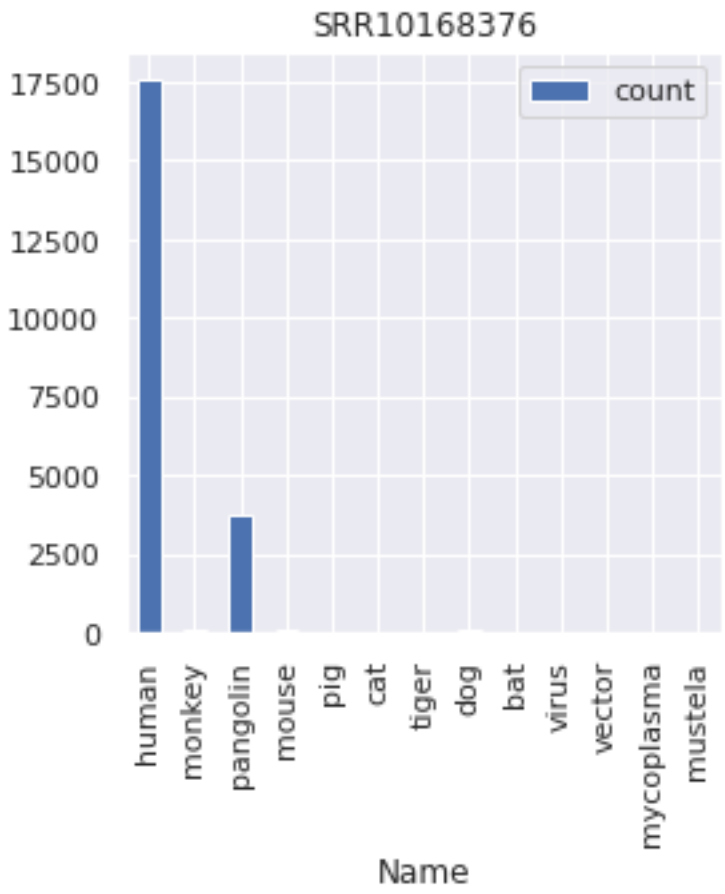
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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12500
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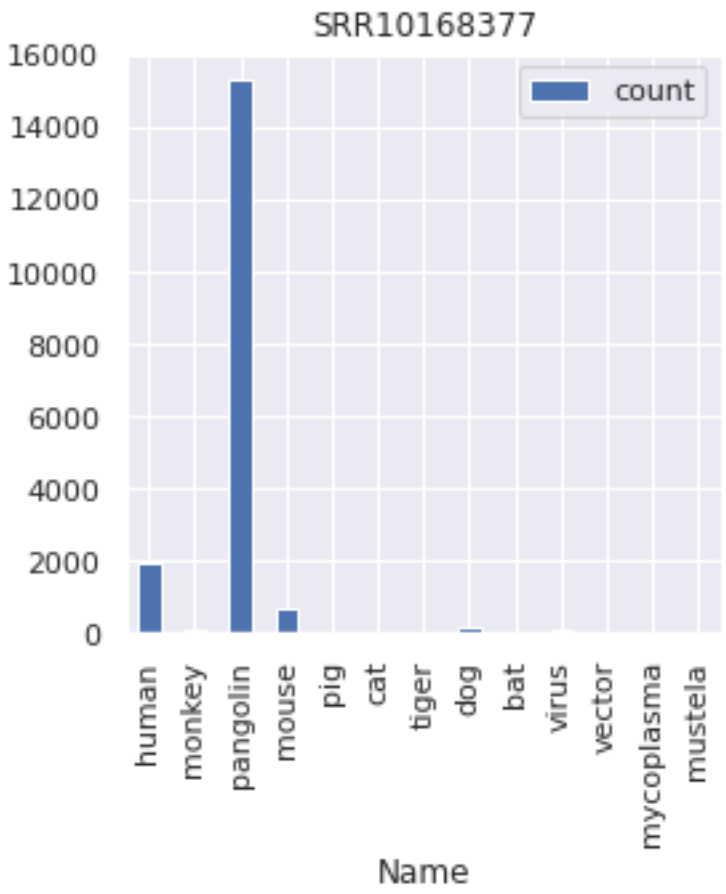
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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14000
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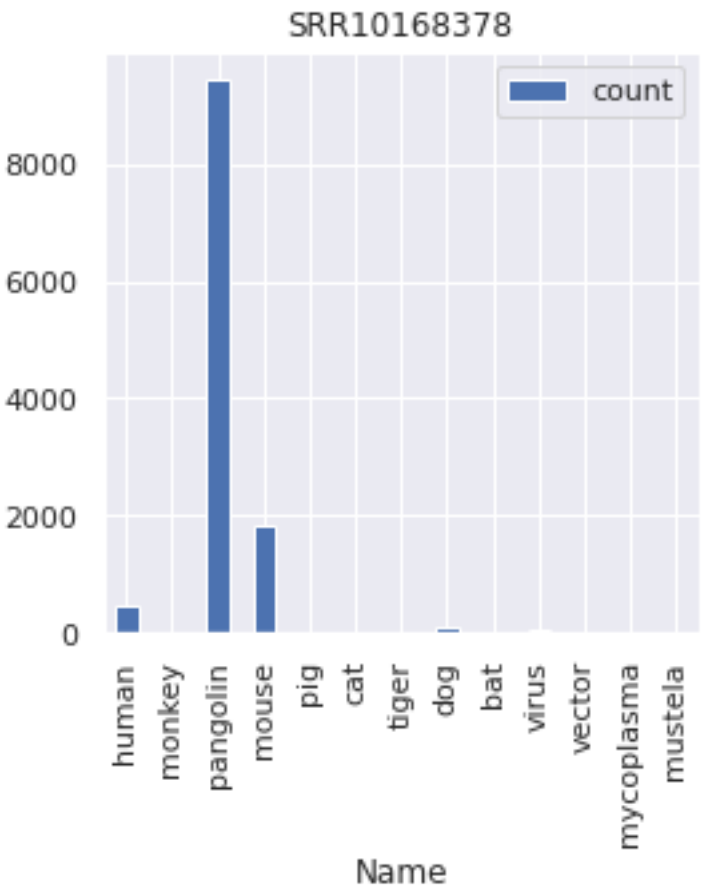
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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count
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6000
4000
2000
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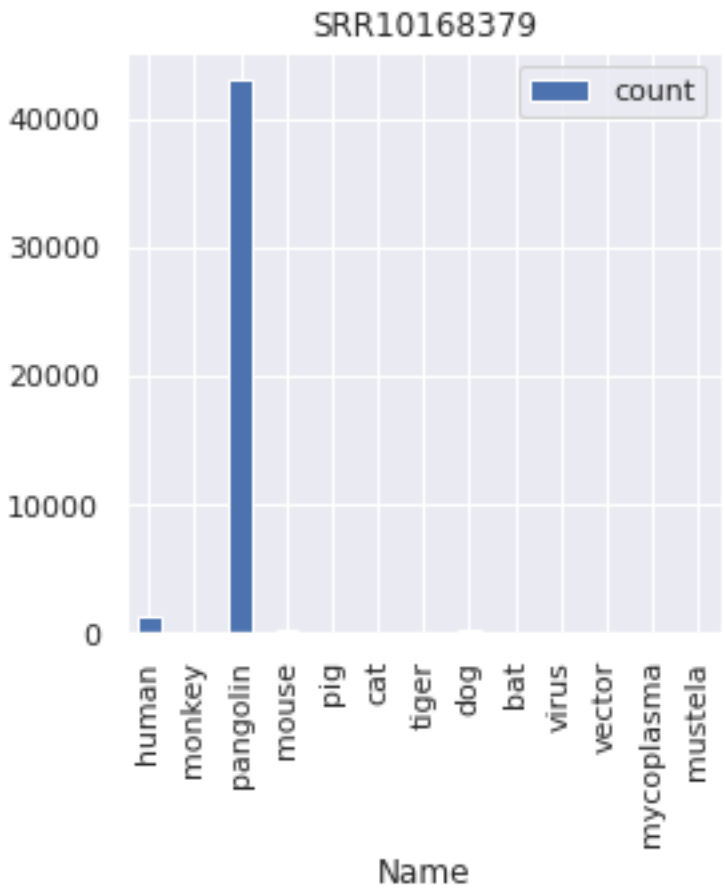
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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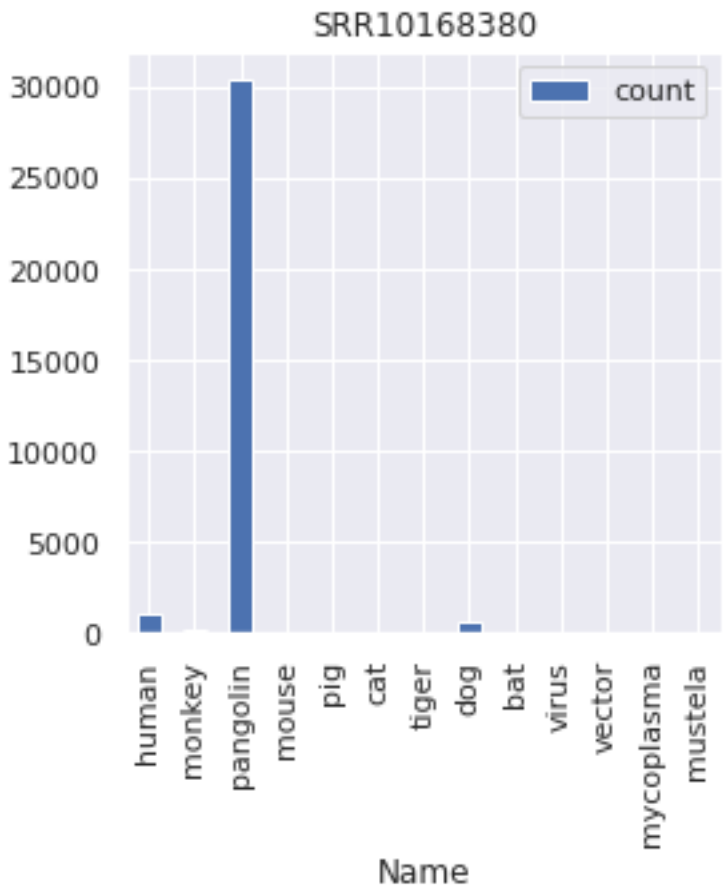
count
40000
30000
20000
10000
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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25000
20000
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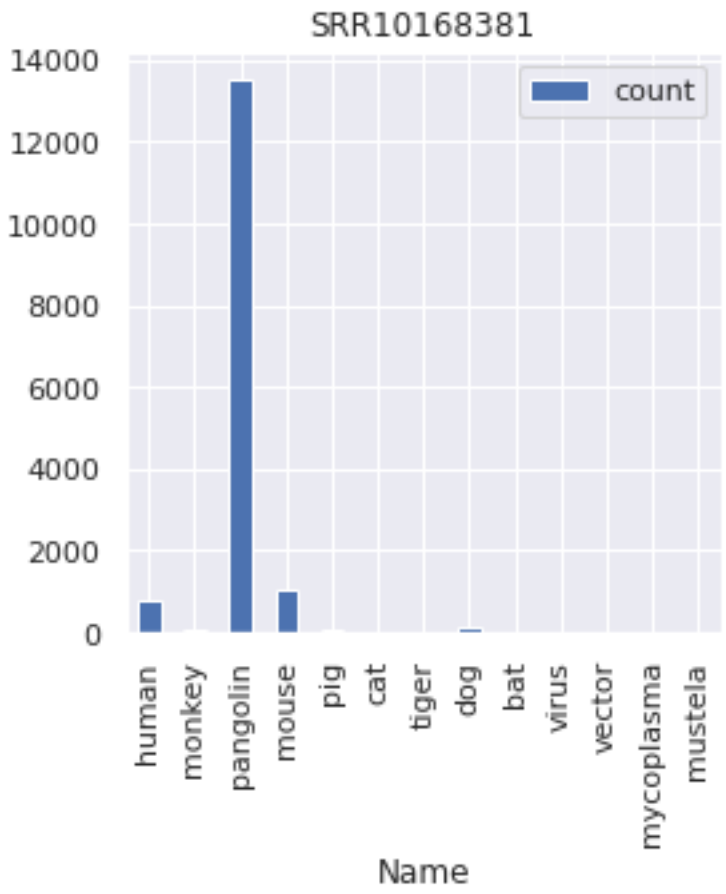
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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12000
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8000
6000
4000
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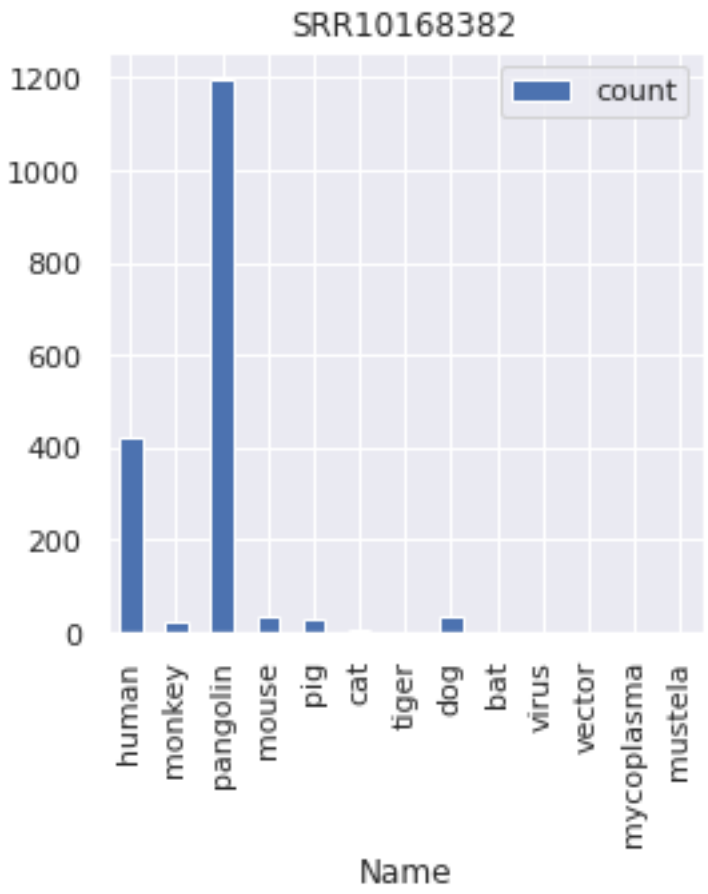
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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1000
800
600
400
200
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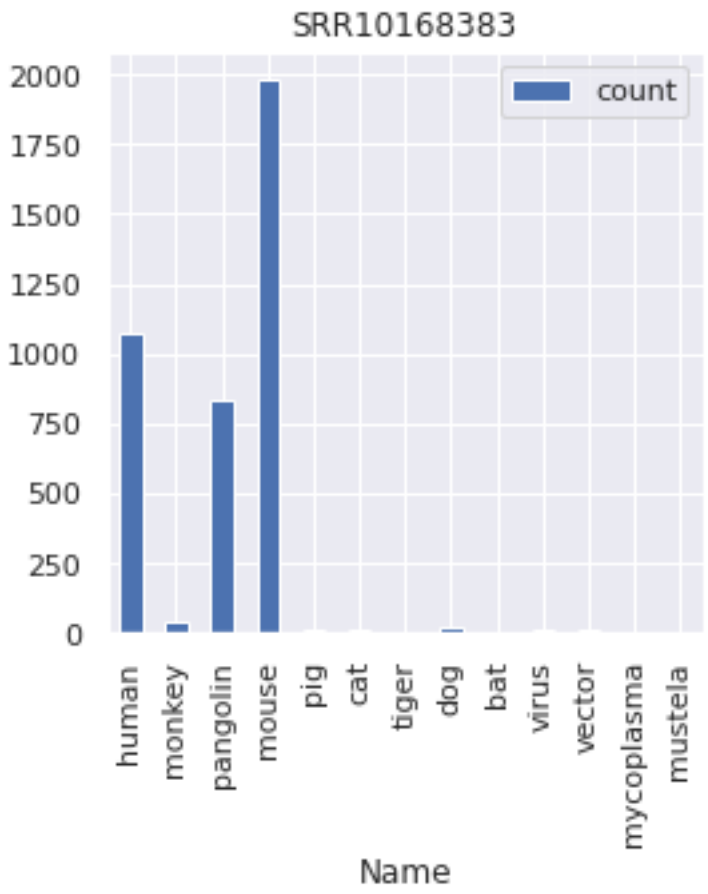
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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1750
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1250
1000
750
500
250
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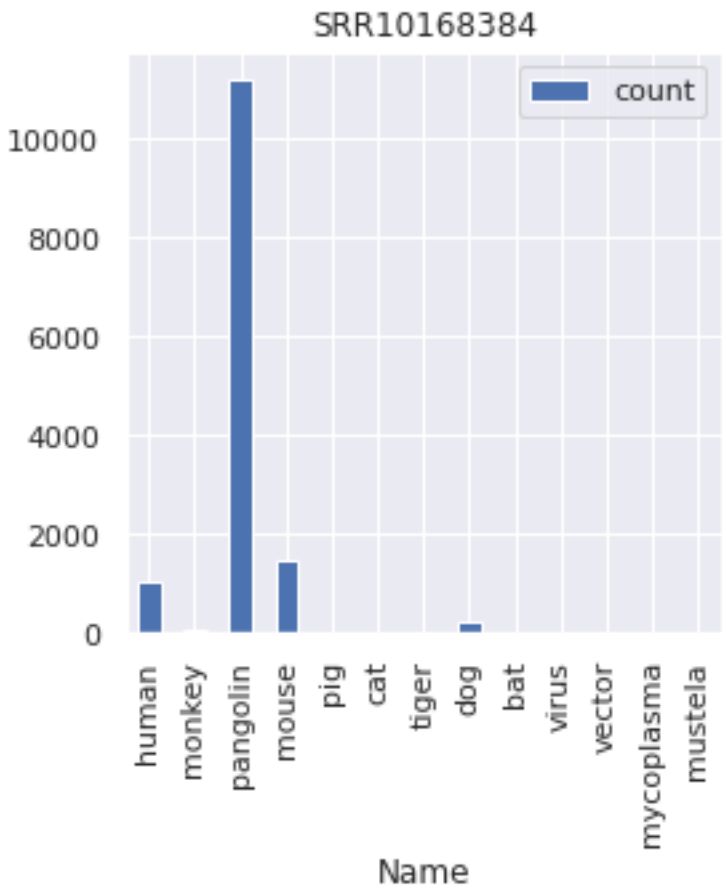
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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count
10000
8000
6000
4000
2000
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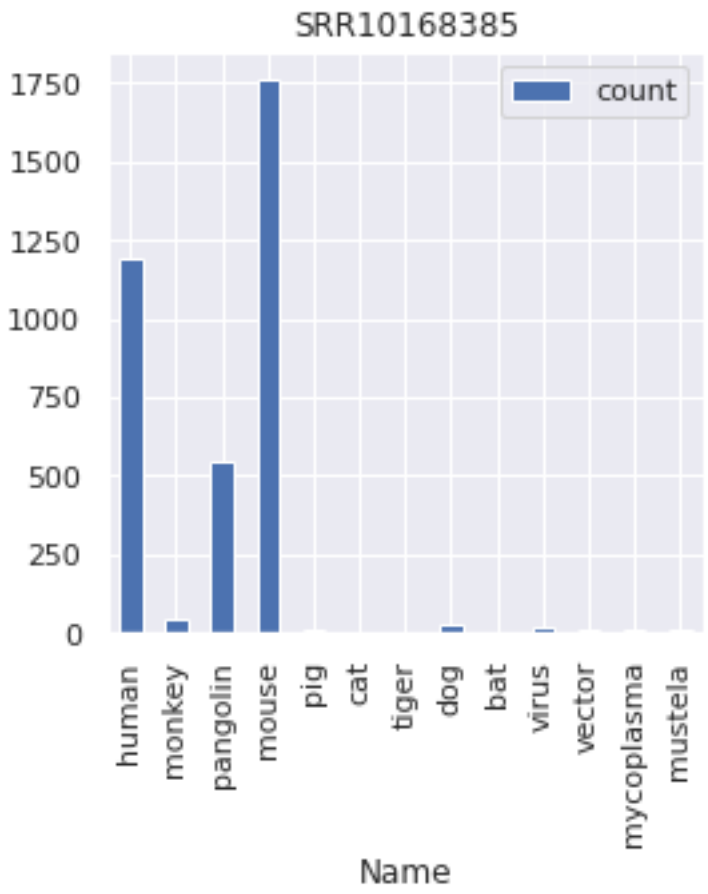
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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1500
1250
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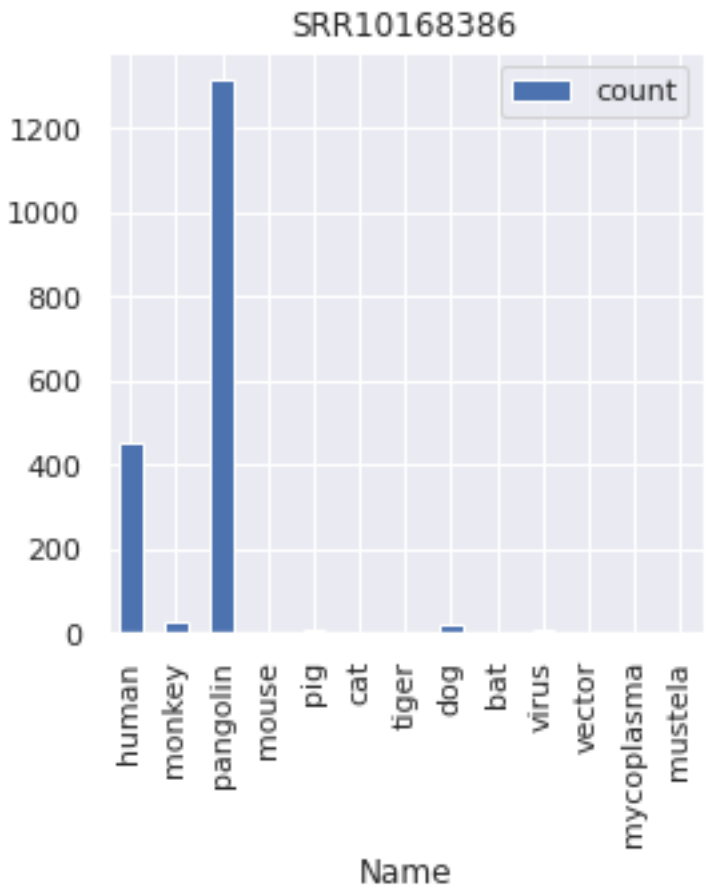
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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count
1200
1000
800
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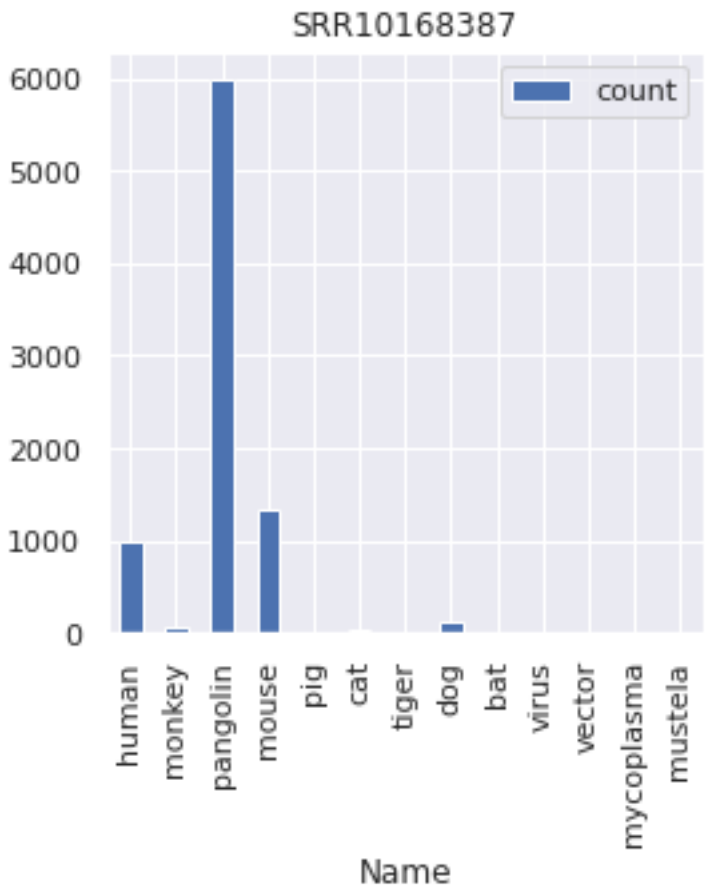
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name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count
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5000
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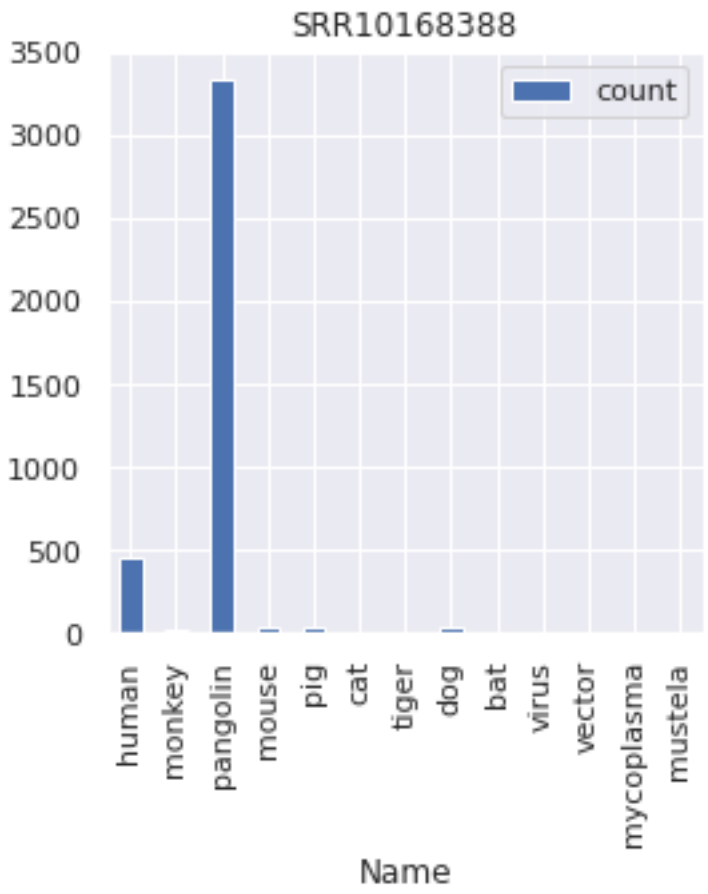
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR10168388
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3000
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pangolin
mouse
pig
cat
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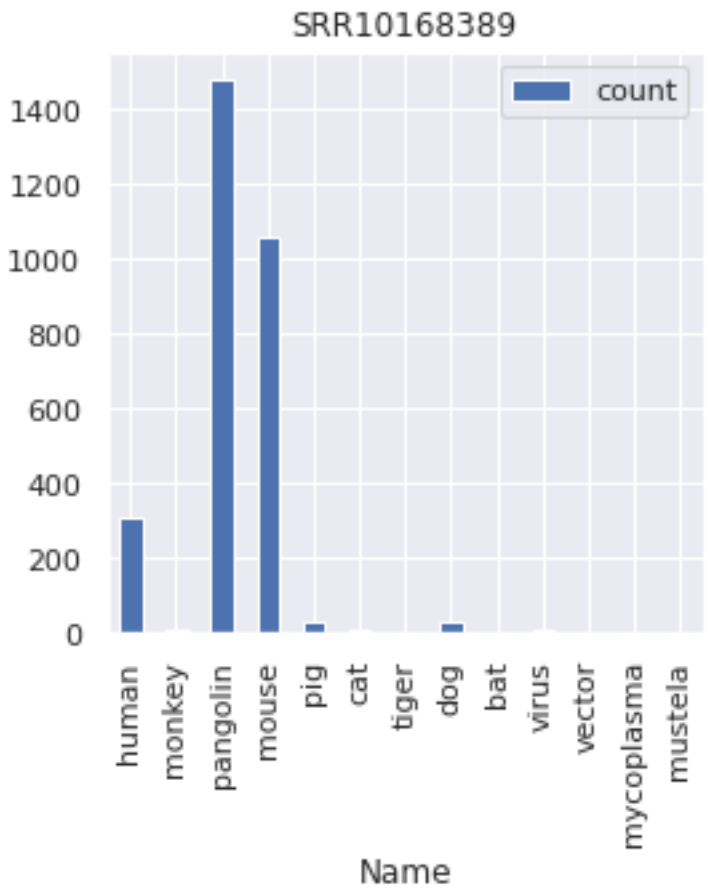
dog
bat
virus
vector
mycoplasma
mustela
Name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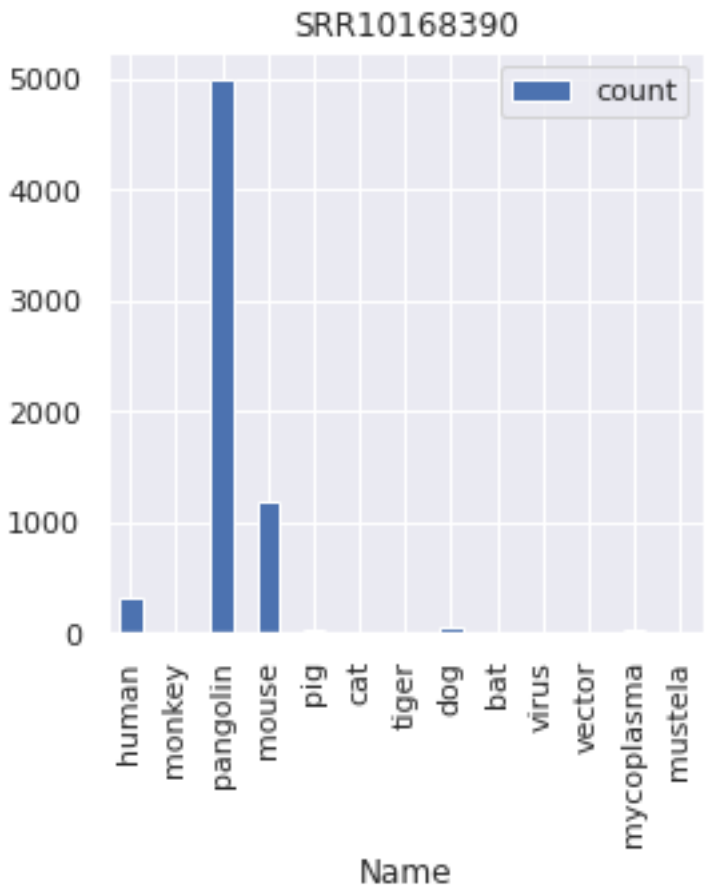
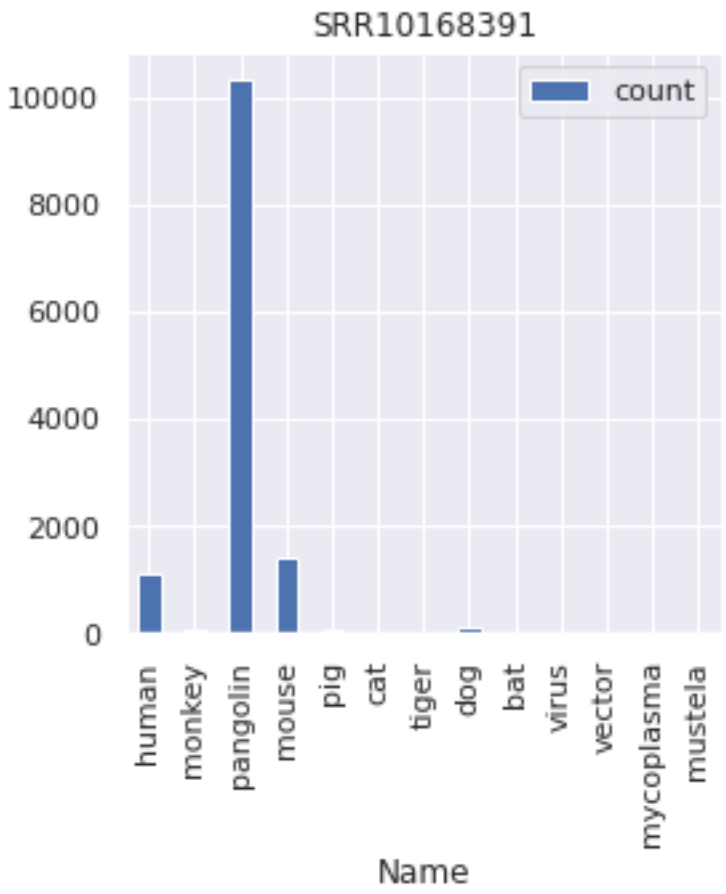
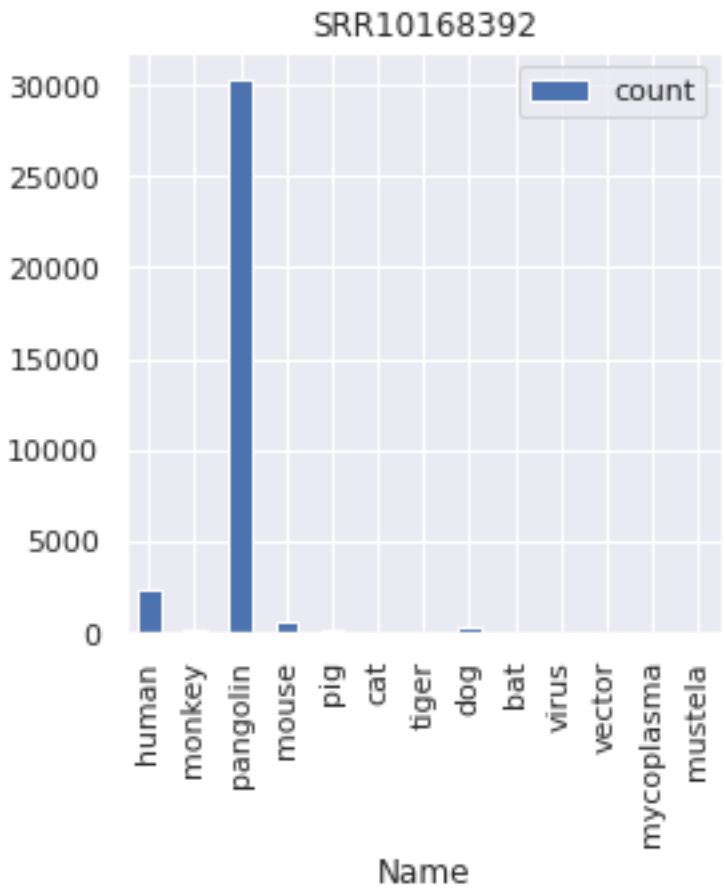
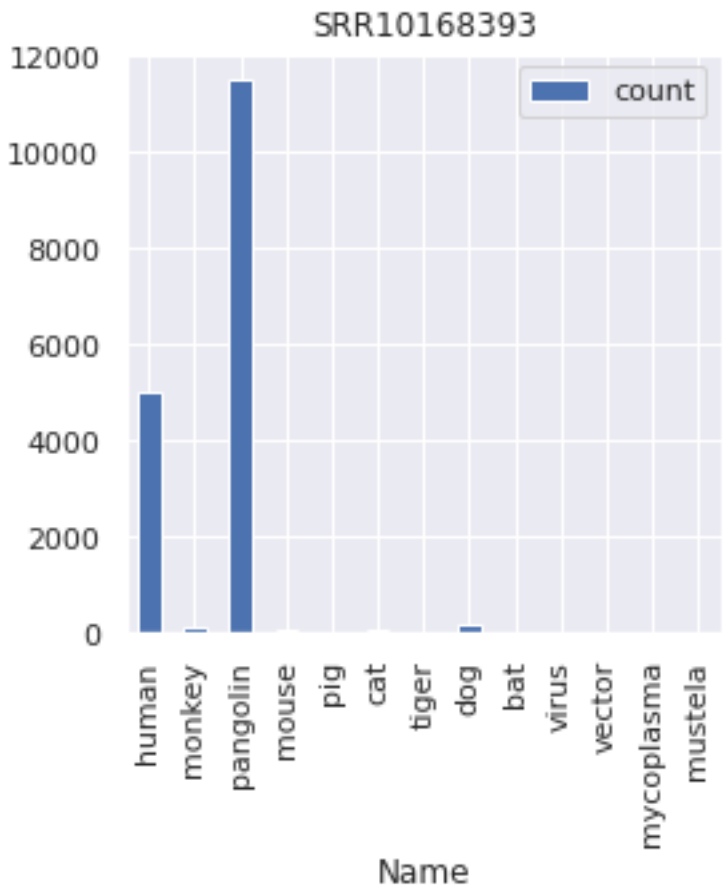
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR10168390
count
5000
4000
3000
2000
1000
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR10168391
count
10000
8000
6000
4000
2000
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR10168392
count
30000
25000
20000
15000
10000
5000
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name



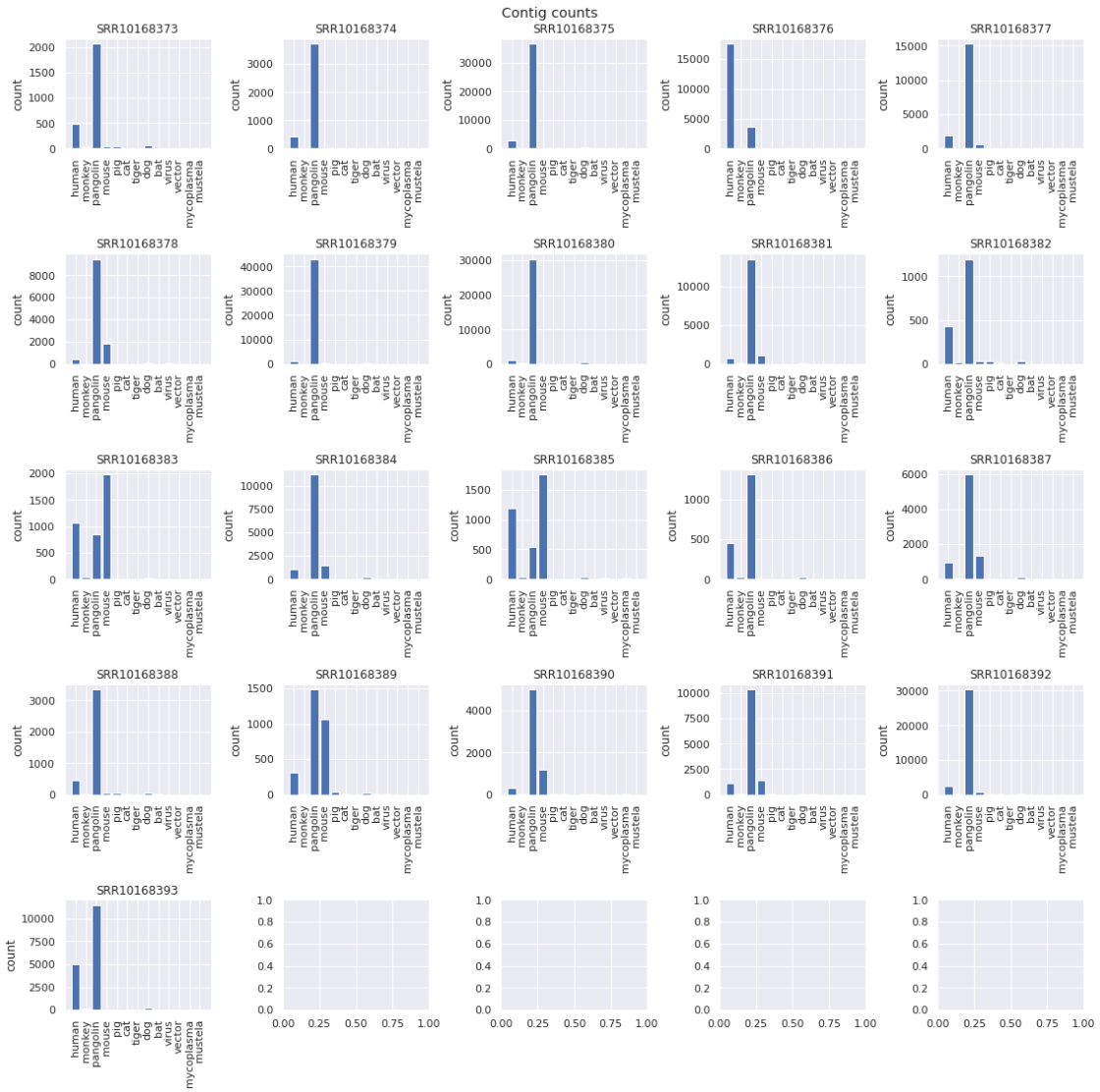
[15]:
```
pathlib.Path(BASE_PATH+'general_plots/').mkdir(exist_ok=True)

def multi_plot():
    fig, axis = plt.subplots(5, 5,figsize=(16,16))
    fig.suptitle('Contig counts')
    n=0
    for r in range(5):
        for c in range(5):
            if n<len(sra_list):
                sra=sra_list[n]
                df=get_descr(sra)
                axis[r,c].bar(df['Name'],df['count'])
                axis[r,c].tick_params(axis='x', rotation=90)
                axis[r,c].set_ylabel('count')
                axis[r,c].title.set_text(sra)
                n+=1

    fig.tight_layout()
```

```
    fig.savefig(BASE_PATH+'general_plots/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_contig_count_matrix.png',␣
↪bbox_inches="tight")
    plt.show()
```

[16]:
```
multi_plot()
```



[17]:
```
frames=[]
for i,sra in enumerate(sra_list):
    try:
        df = pd.read_csv(BASE_PATH+sra+'/magic_blast/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species_df.csv')
```

```
        x = df.Name.astype('category')
        df['species_uid'] =x.cat.codes
        df['SRA_val'] =df.SRA.str.strip('SRR')
        df['SRA_val'] = pd.to_numeric(df['SRA_val'])
        frames.append(df)
    except FileNotFoundError:
        pass
df_sra = pd.concat(frames)
```

[18]:
```
df_sra.drop(columns=['Unnamed: 0'],inplace=True)
```

[19]:
```
df_sra.head(n=100)
```

[19]:

	SRA	Name	count	pct_matched	species_uid	SRA_val
0	SRR10168373	human	486	11.18	3	10168373
1	SRR10168373	monkey	21	0.48	4	10168373
2	SRR10168373	pangolin	2067	47.54	8	10168373
3	SRR10168373	mouse	53	1.22	5	10168373
4	SRR10168373	pig	51	1.17	9	10168373
..	…	…	…	…	…	…
4	SRR10168380	pig	52	0.16	9	10168380
5	SRR10168380	cat	66	0.20	1	10168380
6	SRR10168380	tiger	6	0.02	10	10168380
7	SRR10168380	dog	556	1.67	2	10168380
8	SRR10168380	bat	67	0.20	0	10168380

[100 rows x 6 columns]

[20]:
```
df_sra.Name.unique()
```

[20]:
```
array(['human', 'monkey', 'pangolin', 'mouse', 'pig', 'cat', 'tiger',
       'dog', 'bat', 'virus', 'vector', 'mycoplasma', 'mustela'],
      dtype=object)
```

0.0.3 All nt database matches

[21]:
```
total_dict={}
asc_desc={}
for sra in sra_list:
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    for asc,desc,cnt in zip(accessions,descriptions, counts):
        if asc in total_dict:
            total_dict[asc]+=int(cnt)
        else:
            total_dict[asc]=int(cnt)
        if asc not in asc_desc:
            asc_desc[asc]=desc
```

[22]:
```
assert len(total_dict)==len(asc_desc)
```

[23]:
```
len(asc_desc)
```

[23]:
```
74327
```

Print out the 100 most common nt database classification for all contigs in the project

[24]:
```
def print_top_n_sp(total_dict, max_num):
    listofTuples = sorted(total_dict.items() , reverse=True, key=lambda x: x[1])
    for i, elem in enumerate(listofTuples):
        if i<max_num:
            print(asc_desc[elem[0]], ": " , elem[1] )
        else:
            break
```

[25]:
```
print_top_n_sp(total_dict, max_num=10)
```

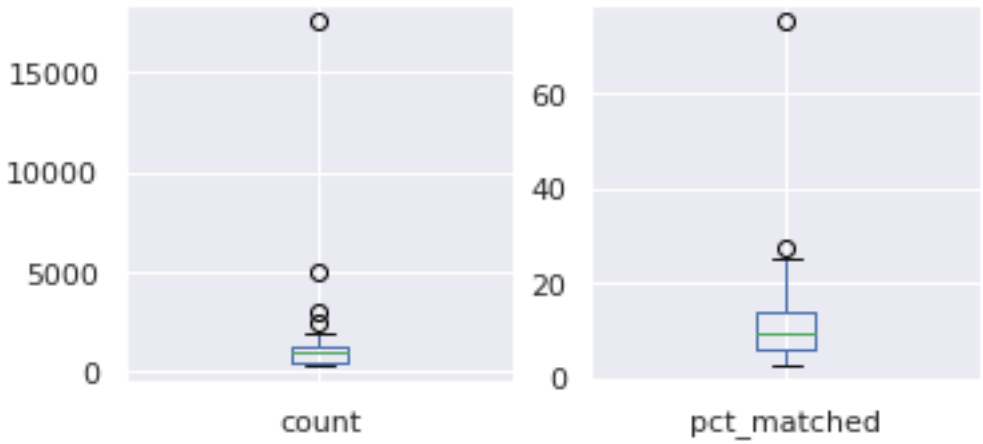
```
Pseudolabrys sp. FHR47 chromosome, complete genome :  858
Eukaryotic synthetic construct chromosome 16 :  841
Homo sapiens DNA, chromosome 16, nearly complete genome :  810
Lutra lutra genome assembly, chromosome: 16 :  656
Eukaryotic synthetic construct chromosome 17 :  554
Staphylococcus aureus strain WH9628 chromosome :  542
Homo sapiens DNA, chromosome 17, nearly complete genome :  527
Sus scrofa 18S ribosomal RNA gene, complete sequence :  516
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome :
507
Homo sapiens clone LA14_101B3 sequence :  506
```

0.0.4 Human

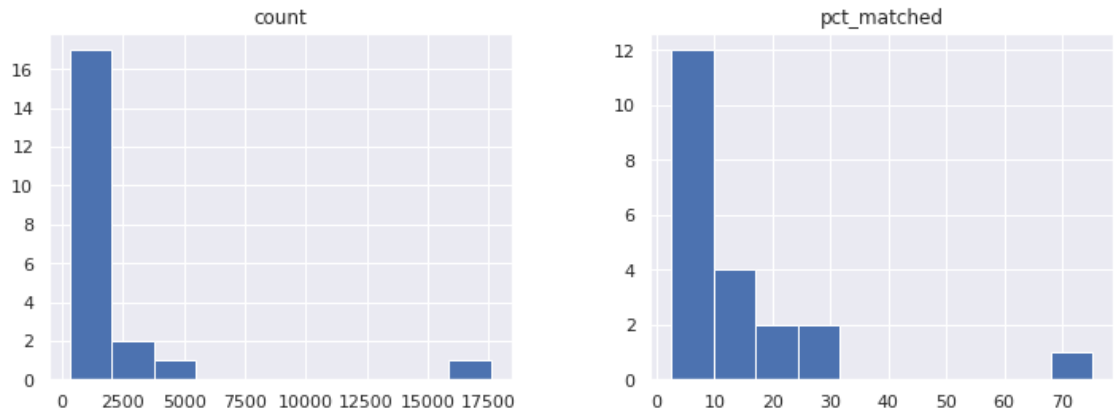
[26]:
```
df=df_sra[df_sra['Name'].str.contains('human')]
```

[27]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

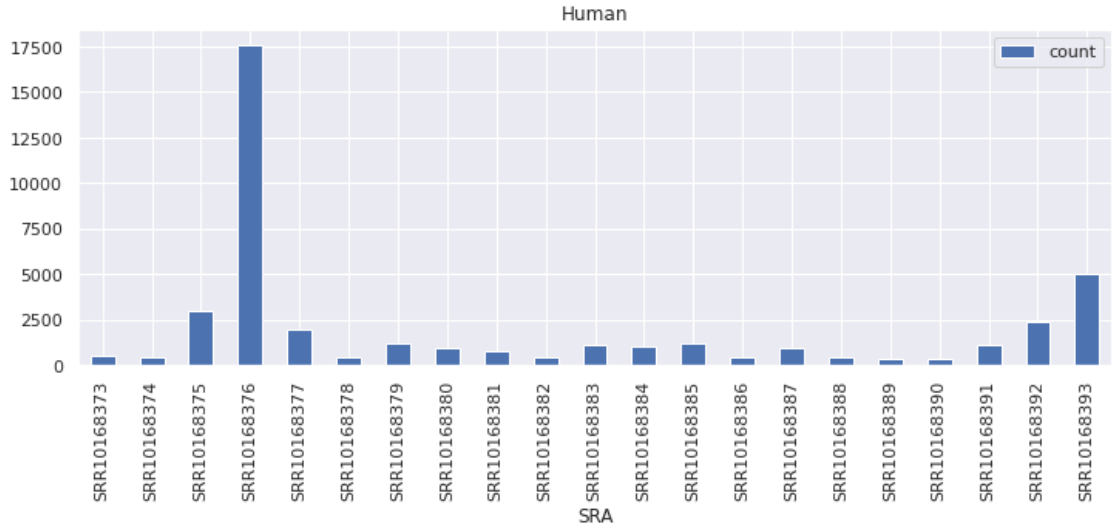
[27]:
```
count            AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



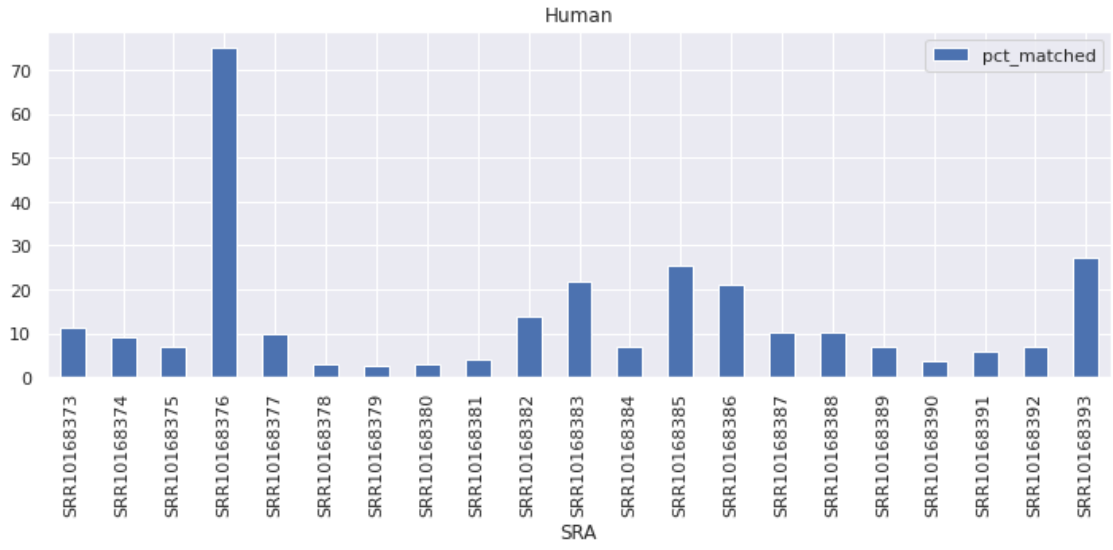
[28]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[29]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title('Human', fontsize=12)
plt.show()
```



[30]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title('Human', fontsize=12)
plt.show()
```



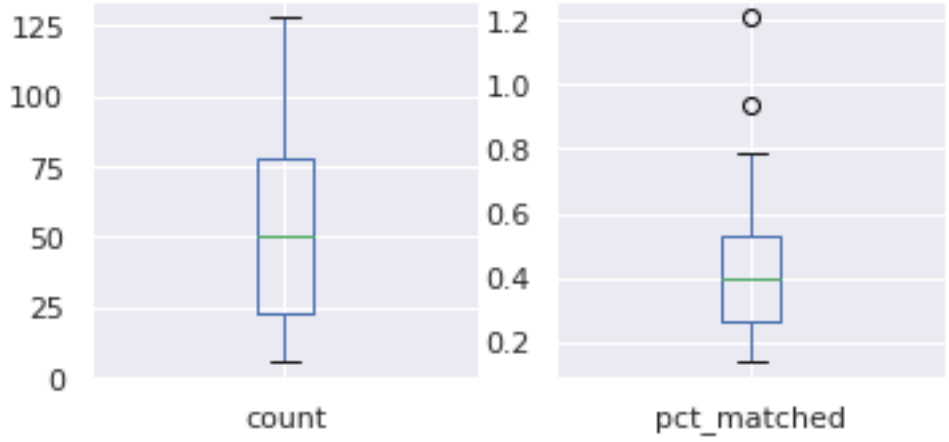
0.0.5 Monkey

[31]:
```
s_name='monkey'
```

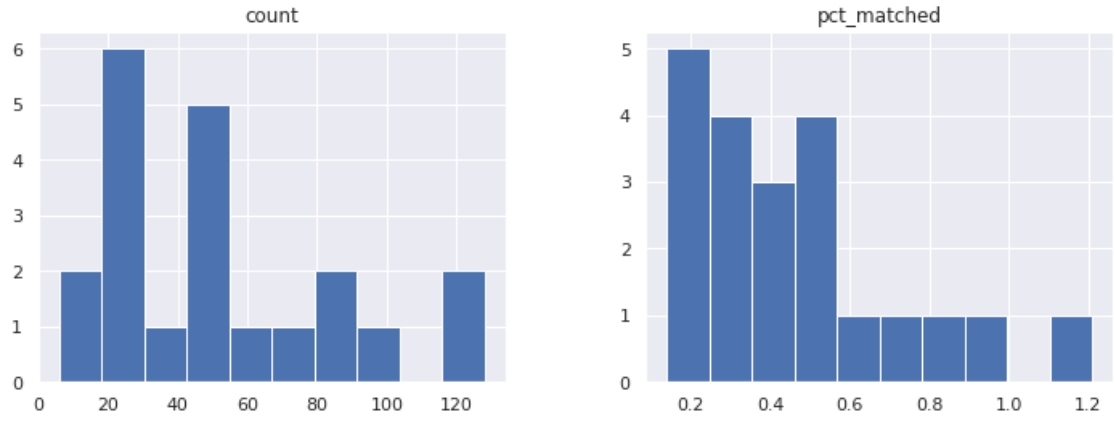
[32]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[33]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

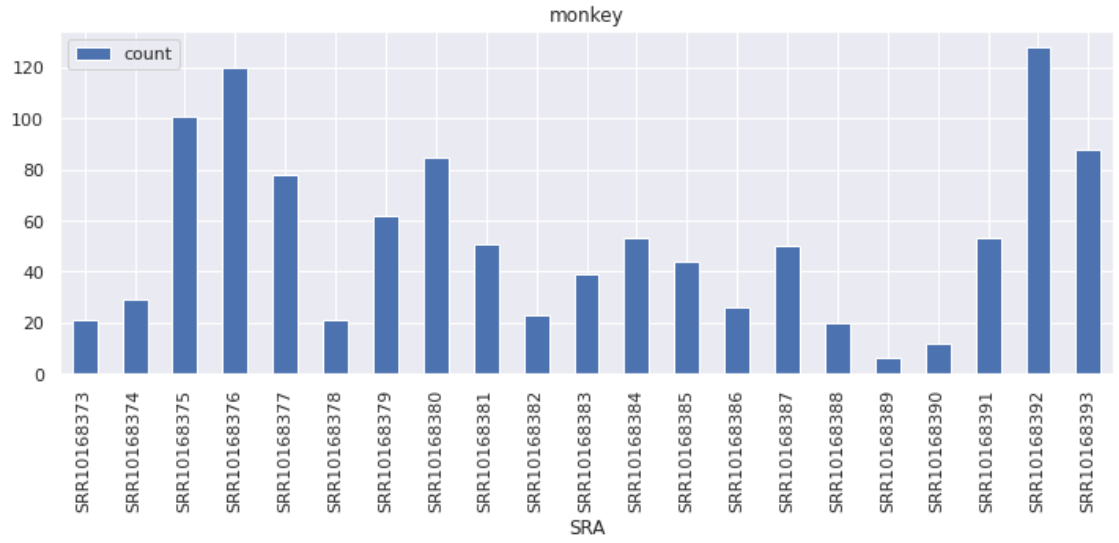
[33]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



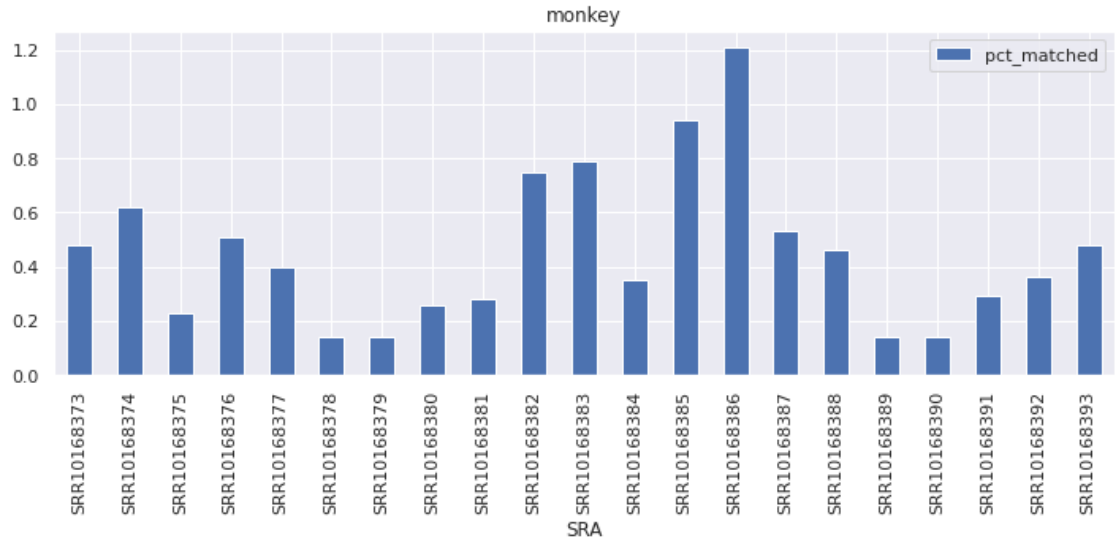
[34]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[35]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[36]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



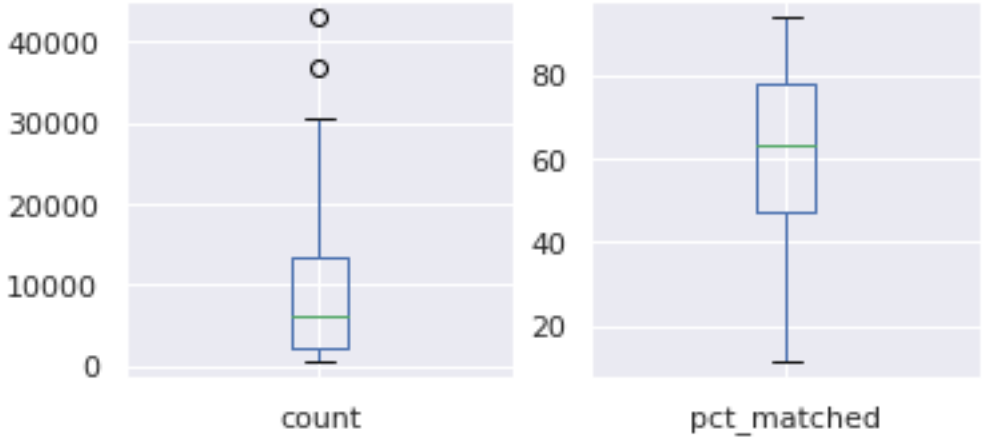
0.0.6 Pangolin

[37]:
```
s_name='pangolin'
```

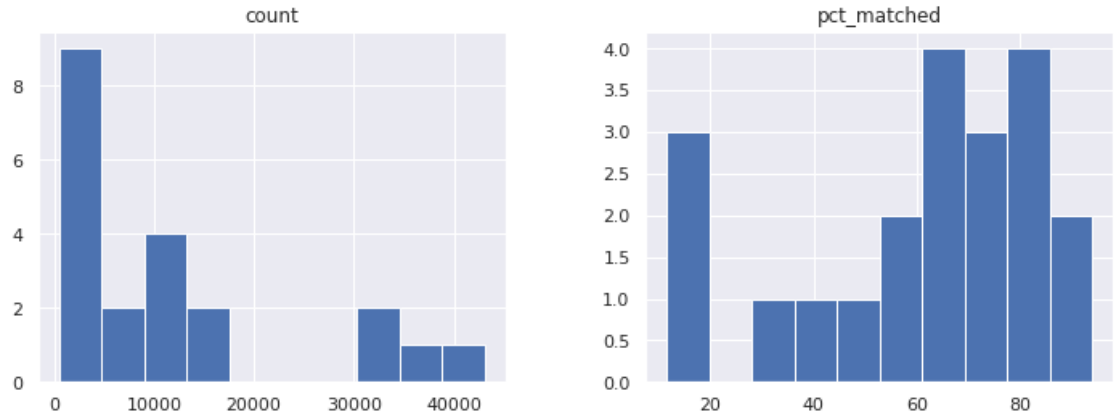
[38]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[39]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
↪sharey=False, figsize=(12,12))
```

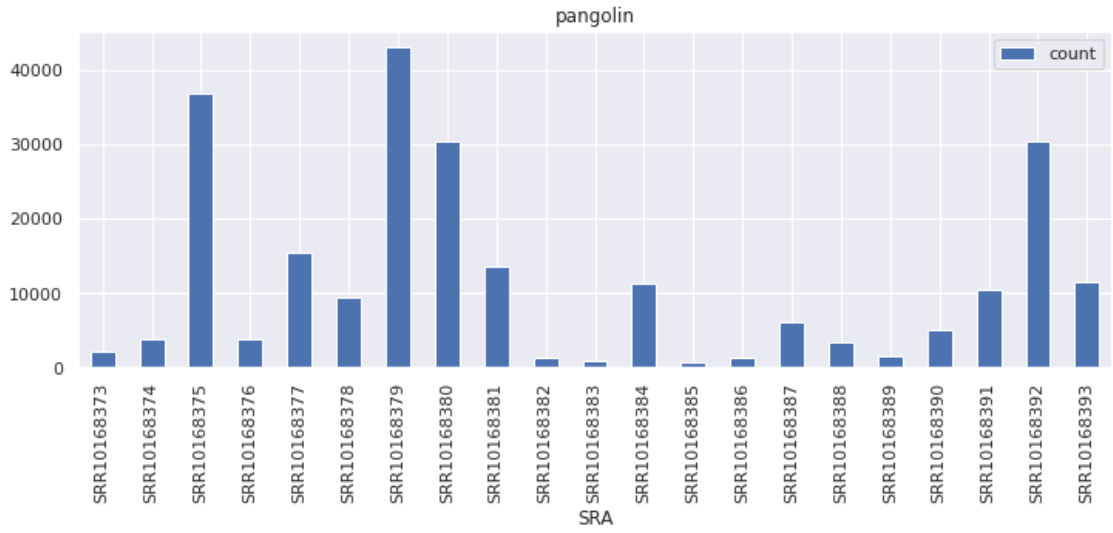
[39]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



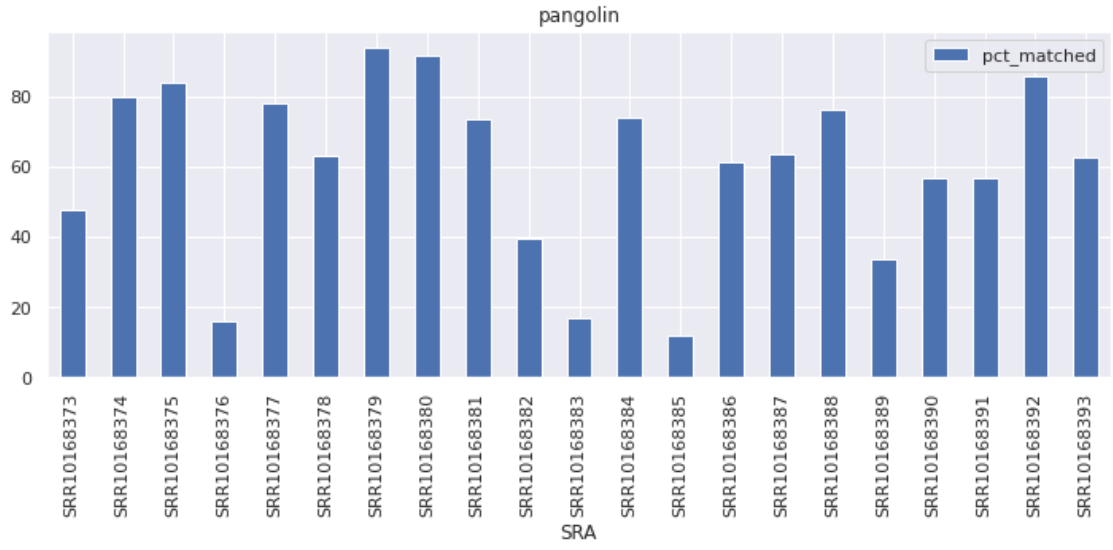
[40]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[41]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[42]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



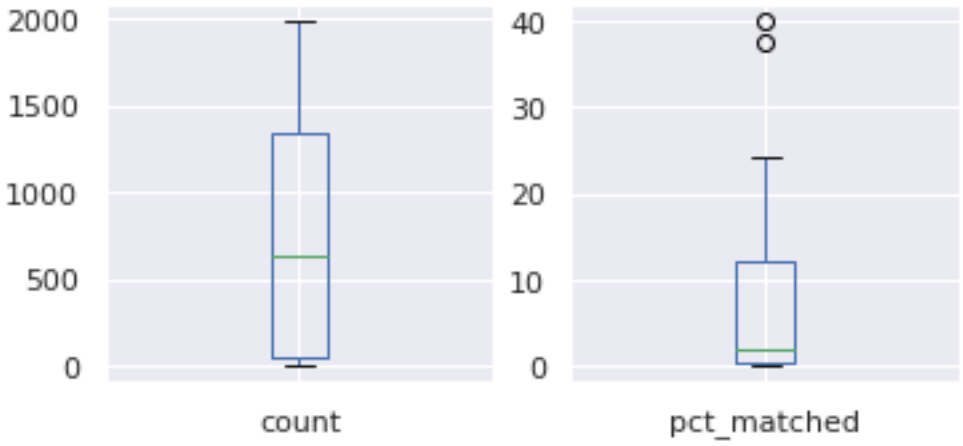
0.0.7 Mouse

[43]:
```
s_name='mouse'
```

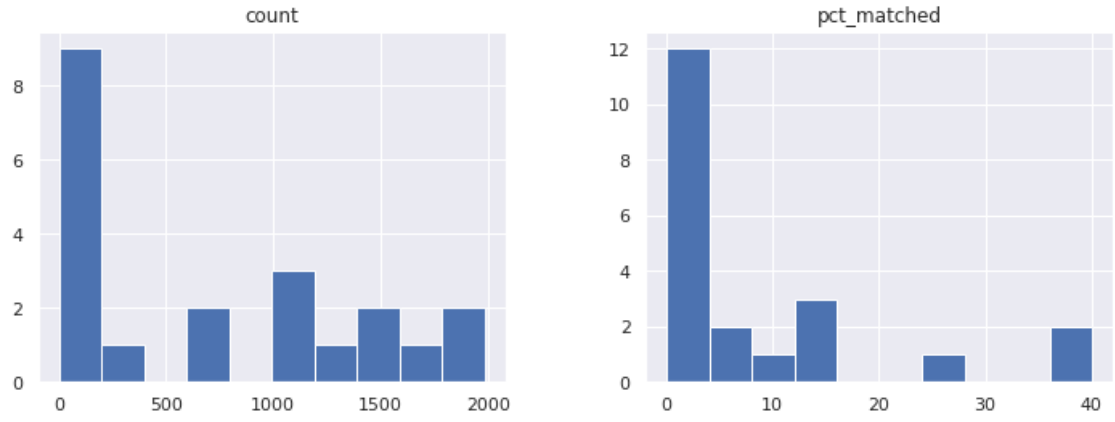
[44]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[45]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

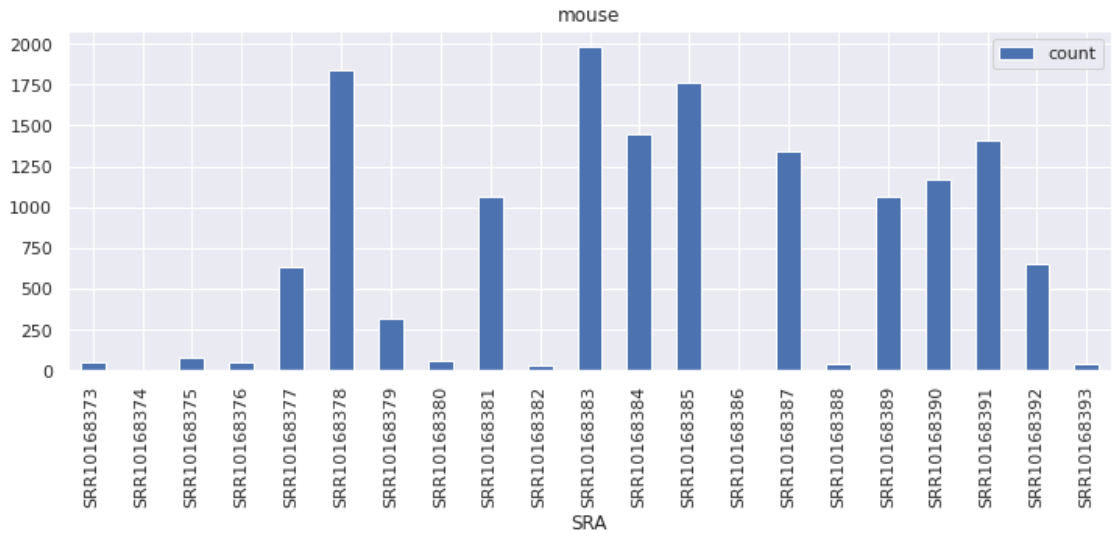
[45]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



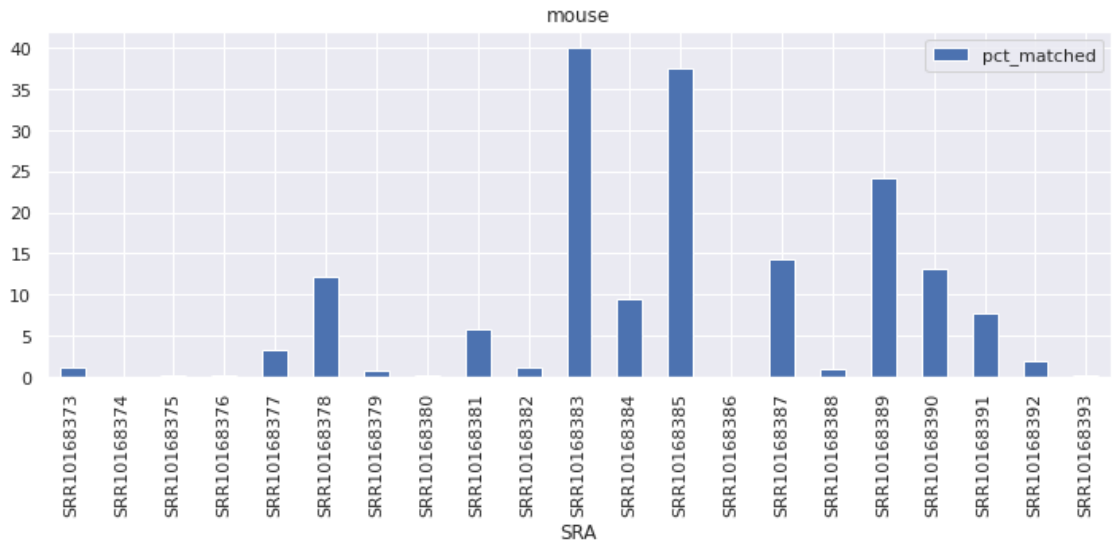
[46]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[47]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[48]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



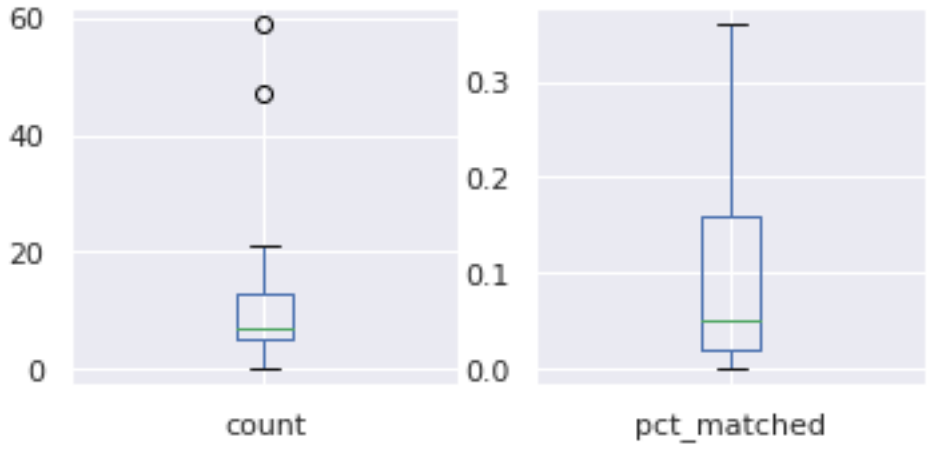
0.0.8 virus

[49]:
```
s_name='virus'
```

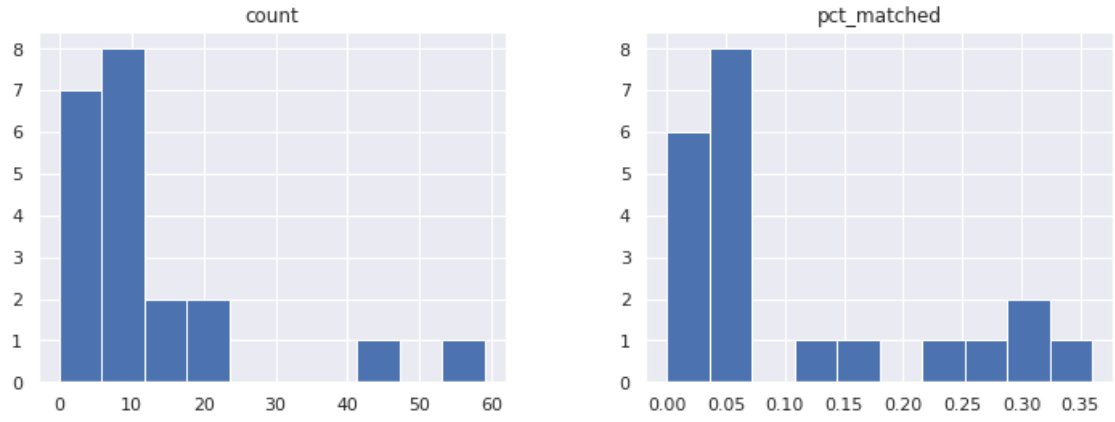
[50]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[51]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
↪sharey=False, figsize=(12,12))
```

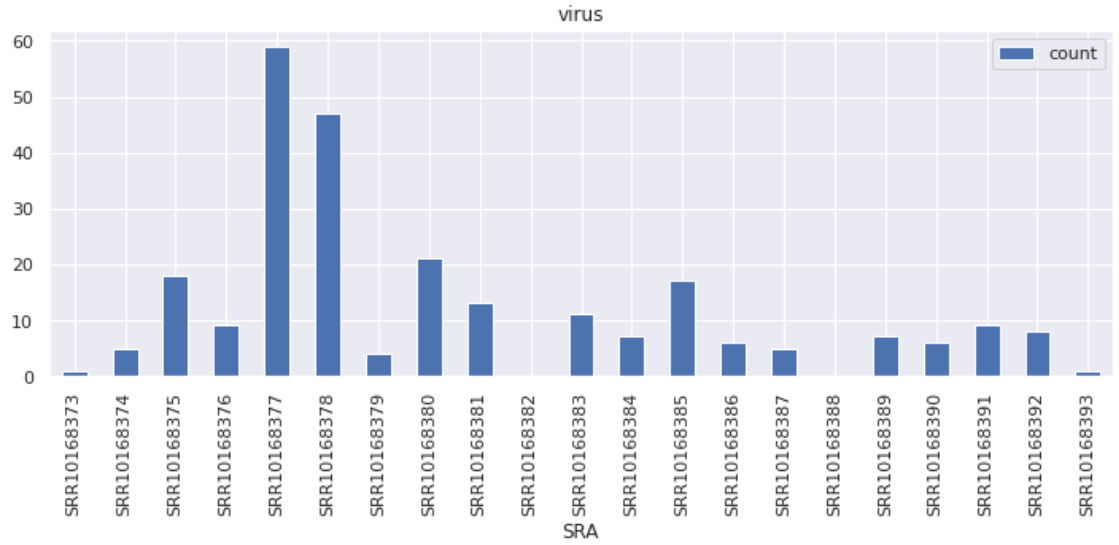
[51]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



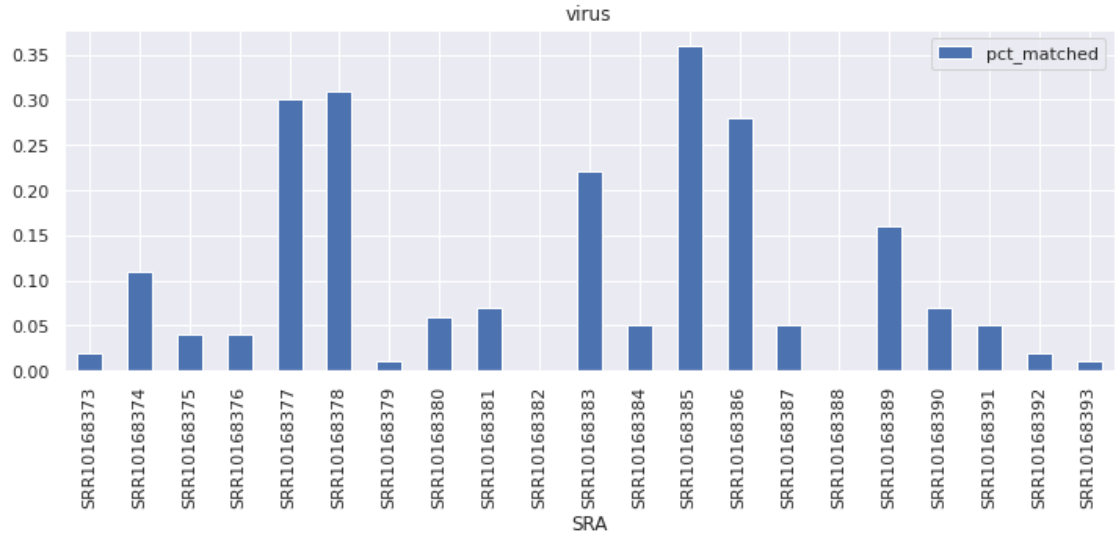
[52]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[53]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[54]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



0.0.9 Top nt database contigs matches per SRA

[55]:
```
def get_sra_dict(sra):
    total_dict={}
    asc_desc={}
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
```

```
    for asc,desc,cnt in zip(accessions,descriptions, counts):
        if asc in total_dict:
            total_dict[asc]+=int(cnt)
        else:
            total_dict[asc]=int(cnt)
        if asc not in asc_desc:
            asc_desc[asc]=desc
    return total_dict, asc_desc, total
```

[56]:
```
for sra in sra_list:
    total_dict, asc_desc, total= get_sra_dict(sra)
    print(f'{sra}, number of contigs {total}')
    print_top_n_sp(total_dict, max_num=10)
    print('\n')
```

```
SRR10168373, number of contigs 2117
Manis javanica isolate EP2 mitochondrion, complete genome :  151
Manis javanica isolate T298 mitochondrion, complete genome :  150
Manis javanica isolate MJA633 mitochondrion, complete genome :  140
Manis pentadactyla mitochondrion, complete genome :  101
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome :  100
Sphingomonas paucimobilis strain FDAARGOS_908 chromosome, complete genome :  62
Sphingomonas paucimobilis strain FDAARGOS_881 chromosome, complete genome :  58
Lutra lutra genome assembly, chromosome: 16 :  50
Sphingomonas sp. LK11, complete genome :  49
Staphylococcus aureus strain WH9628 chromosome :  49


SRR10168374, number of contigs 3784
Fusobacterium varium ATCC 27725 chromosome, complete genome :  10
Fusobacterium varium strain NCTC10560 genome assembly, chromosome: 1 :  10
Fusobacterium ulcerans ATCC 49185 isolate Fusobacterium ulcerans 81A6 genome
assembly, chromosome: 1 :  10
PREDICTED: Manis javanica AHNAK nucleoprotein (AHNAK), mRNA :  10
Fusobacterium ulcerans strain NCTC12112 genome assembly, chromosome: 1 :  9
Peptostreptococcus anaerobius ATCC:27337 16S-23S ribosomal intergenic spacer and
23S ribosomal RNA gene, partial sequence :  8
Fusobacterium varium Fv113-g1 DNA, complete genome :  7
Acinetobacter towneri strain 19110F47 chromosome, complete genome :  7
PREDICTED: Manis javanica thrombospondin 1 (THBS1), mRNA :  7
Staphylococcus condimenti strain DSM 11674, complete genome :  6


SRR10168375, number of contigs 24599
Homo sapiens DNA, chromosome 16, nearly complete genome :  153
Eukaryotic synthetic construct chromosome 16 :  151
Homo sapiens interleukin 9 receptor (IL9Rps) pseudogene, complete sequence; and
```

DNA-directed RNA polymerases III 12.5 kDa polypeptide (POLR3K), U11/U12 snRNP 25 kDa protein (C16orf33), RHBDG1 (C16orf8), DNA-3-methyladenine glycosylase (MPG), -14 gene protein (C16orf35), hemoglobin zeta subunit (HBZ), HBD (HBD), alpha globin (HBA2), alpha globin (HBA1), theta globin (HBQ1), and putative RNA-binding protein Luc7-like 1 (LUC7L) genes, complete cds : 73
Homo sapiens 16p13.3 sequence section 1 of 8 : 70
Homo sapiens 16p13.3 sequence section 2 of 8 : 60
Propionibacterium acnes TypeIA2 P.acn17, complete genome : 60
Propionibacterium acnes TypeIA2 P.acn31, complete genome : 58
Cutibacterium acnes TP-CU389 DNA, complete genome : 56
Propionibacterium acnes TypeIA2 P.acn33, complete genome : 56
Lutra lutra genome assembly, chromosome: 16 : 53

SRR10168376, number of contigs 7147
Eukaryotic synthetic construct chromosome 16 : 414
Homo sapiens DNA, chromosome 16, nearly complete genome : 382
Eukaryotic synthetic construct chromosome 19 : 297
Eukaryotic synthetic construct chromosome 17 : 292
Homo sapiens DNA, chromosome 17, nearly complete genome : 289
Homo sapiens DNA, chromosome 19, nearly complete genome : 272
Eukaryotic synthetic construct chromosome 19 : 158
Homo sapiens titin (TTN) gene, complete cds : 115
Homo sapiens DNA, chromosome 20, nearly complete genome : 114
Homo sapiens DNA, chromosome 15, nearly complete genome : 113

SRR10168377, number of contigs 13755
Psychrobacter sp. PRwf-1 chromosome, complete genome : 21
Eukaryotic synthetic construct chromosome 17 : 21
Lutra lutra genome assembly, chromosome: 16 : 21
Homo sapiens DNA, chromosome 17, nearly complete genome : 21
Pangolin coronavirus isolate MP789, complete genome : 20
Staphylococcus aureus strain WH9628 chromosome : 18
PREDICTED: Manis javanica AHNAK nucleoprotein (AHNAK), mRNA : 18
Sus scrofa 18S ribosomal RNA gene, complete sequence : 18
Homo sapiens clone LA14_101B3 sequence : 18
Mouse DNA sequence from clone RP23-81C12 on chromosome 17, complete sequence : 18

SRR10168378, number of contigs 11263
Sporosarcina ureilytica strain LMG 22257 chromosome, complete genome : 55
Sporosarcina pasteurii strain BNCC 337394 chromosome, complete genome : 35
Staphylococcus arlettae P2 DNA, complete genome : 34
Bacillus sp. OxB-1 DNA, complete genome : 31
Vagococcus carniphilus strain ATCC BAA-640 chromosome, complete genome : 30
Hathewaya histolytica strain NCTC503 genome assembly, chromosome: 1 : 25

Savagea faecisuis strain Tyl34 23S ribosomal RNA gene, partial sequence : 24
Savagea faecisuis strain Tyl40 23S ribosomal RNA gene, partial sequence : 24
Psychrobacter sp. PRwf-1 chromosome, complete genome : 22
Lutra lutra genome assembly, chromosome: 16 : 21

SRR10168379, number of contigs 25159
PREDICTED: Manis javanica AHNAK nucleoprotein (AHNAK), mRNA : 33
Roseomonas mucosa strain AD2 chromosome, complete genome : 27
Lutra lutra genome assembly, chromosome: 16 : 25
Roseomonas mucosa strain FDAARGOS_658 chromosome 4, complete sequence : 23
Roseomonas sp. FDAARGOS_362 chromosome, complete genome : 21
PREDICTED: Manis javanica dystonin (DST), transcript variant X2, mRNA : 20
PREDICTED: Manis javanica igE-binding protein-like (LOC118971992), partial mRNA : 18
PREDICTED: Manis javanica dystonin (DST), transcript variant X3, mRNA : 18
PREDICTED: Manis javanica dystonin (DST), transcript variant X4, mRNA : 18
PREDICTED: Manis javanica dystonin (DST), transcript variant X5, mRNA : 18

SRR10168380, number of contigs 19957
Lutra lutra genome assembly, chromosome: 16 : 49
Homo sapiens clone N29M24 sequence : 37
Homo sapiens clone LA14_101B3 sequence : 37
Homo sapiens clone LA13_165F6 sequence : 37
Mus musculus clone contig 1 chromocenter region genomic sequence : 36
Staphylococcus aureus strain WH9628 chromosome : 36
Homo sapiens clone LA15_25H3 sequence : 36
Ovis canadensis canadensis isolate 43U chromosome 24 sequence : 36
Sus scrofa 18S ribosomal RNA gene, complete sequence : 35
Human DNA sequence from clone bP-2171C21 on chromosome 21, complete sequence : 35

SRR10168381, number of contigs 11914
Paeniclostridium sordellii strain AM370 chromosome, complete genome : 196
Clostridiaceae bacterium 14S0207 chromosome, complete genome : 110
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome : 74
Edwardsiella tarda strain KC-Pc-HB1 chromosome, complete genome : 64
Flavobacterium sp. xlx-214 chromosome, complete genome : 59
Neobacillus thermocopriae strain DUT50_236 chromosome, complete genome : 56
Beta vulgaris chloroplast sequence : 55
Plesiomonas shigelloides strain NCTC10360 genome assembly, chromosome: 1 : 52
Plesiomonas shigelloides strain MS-17-188 chromosome, complete genome : 52
Romboutsia ilealis strain CRIB genome assembly, chromosome: chr1 : 51

SRR10168382, number of contigs 1683
Pseudolabrys sp. FHR47 chromosome, complete genome : 857
Lutra lutra genome assembly, chromosome: 16 : 33
Mus musculus clone contig 1 chromocenter region genomic sequence : 29
Staphylococcus aureus strain WH9628 chromosome : 29
Sus scrofa 18S ribosomal RNA gene, complete sequence : 29
Human DNA sequence from clone bP-2171C21 on chromosome 21, complete sequence : 29
Homo sapiens clone N29M24 sequence : 29
Homo sapiens clone LA15_25H3 sequence : 29
Homo sapiens clone LA14_101B3 sequence : 29
Homo sapiens clone LA13_165F6 sequence : 29

SRR10168383, number of contigs 3991
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome : 97
Beta vulgaris chloroplast sequence : 72
Eukaryotic synthetic construct chromosome 17 : 17
Homo sapiens DNA, chromosome 17, nearly complete genome : 16
Beta vulgaris subsp. vulgaris mitochondrial DNA, complete genome : 13
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome : 12
Manis javanica isolate EP2 mitochondrion, complete genome : 12
Manis javanica isolate T298 mitochondrion, complete genome : 12
Manis javanica isolate MJA633 mitochondrion, complete genome : 11
Myroides phaeus strain 18QD1AZ29W chromosome, complete genome : 11

SRR10168384, number of contigs 11723
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome : 74
Beta vulgaris chloroplast sequence : 53
Lutra lutra genome assembly, chromosome: 16 : 26
Mus musculus clone contig 1 chromocenter region genomic sequence : 21
Staphylococcus aureus strain WH9628 chromosome : 21
Sus scrofa 18S ribosomal RNA gene, complete sequence : 21
Human DNA sequence from clone bP-2171C21 on chromosome 21, complete sequence : 21
Homo sapiens clone N29M24 sequence : 21
Homo sapiens clone LA15_25H3 sequence : 21
Homo sapiens clone LA14_101B3 sequence : 21

SRR10168385, number of contigs 3661
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome : 94
Beta vulgaris chloroplast sequence : 71
Acinetobacter bereziniae strain GD0320 chromosome, complete genome : 32

Acinetobacter bereziniae strain GD03185 chromosome, complete genome : 21
Clostridiaceae bacterium 14S0207 chromosome, complete genome : 19
Beta macrocarpa mitochondrion, complete genome : 18
Acinetobacter bereziniae strain XH901, complete genome : 17
Beta vulgaris subsp. maritima genotype male-fertile B mitochondrion, complete genome : 17
Beta vulgaris subsp. maritima genotype male-fertile A mitochondrion, complete genome : 16
Beta vulgaris subsp. vulgaris mitochondrial DNA, complete genome : 15

SRR10168386, number of contigs 1870
Manis javanica isolate EP2 mitochondrion, complete genome : 24
Manis javanica isolate T298 mitochondrion, complete genome : 24
Manis javanica isolate MJA633 mitochondrion, complete genome : 21
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome : 13
Homo sapiens DNA, sequence_id: unplaced_0471 : 13
Paeniclostridium sordellii strain AM370 chromosome, complete genome : 12
Manis pentadactyla mitochondrion, complete genome : 9
Clostridium isatidis strain DSM 15098 chromosome, complete genome : 8
Homo sapiens DNA, sequence_id: unplaced_0335 : 7
Eukaryotic synthetic construct chromosome 15 : 6

SRR10168387, number of contigs 7626
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome : 77
Beta vulgaris chloroplast sequence : 56
Lutra lutra genome assembly, chromosome: 16 : 19
Staphylococcus aureus strain WH9628 chromosome : 14
Acinetobacter bereziniae strain GD0320 chromosome, complete genome : 13
Mus musculus clone contig 1 chromocenter region genomic sequence : 12
Eukaryotic synthetic construct chromosome 17 : 12
Beta vulgaris subsp. maritima genotype male-fertile B mitochondrion, complete genome : 12
Manis pentadactyla mitochondrion, complete genome : 12
Sus scrofa 18S ribosomal RNA gene, complete sequence : 12

SRR10168388, number of contigs 3512
Lutra lutra genome assembly, chromosome: 16 : 42
Mus musculus clone contig 1 chromocenter region genomic sequence : 39
Staphylococcus aureus strain WH9628 chromosome : 39
Human DNA sequence from clone bP-2171C21 on chromosome 21, complete sequence : 39
Homo sapiens clone N29M24 sequence : 39
Homo sapiens clone LA15_25H3 sequence : 39
Homo sapiens clone LA14_101B3 sequence : 39

Homo sapiens clone LA13_165F6 sequence : 39
Mouse DNA sequence from clone RP23-81C12 on chromosome 17, complete sequence :
39
Ovis canadensis canadensis isolate 43U chromosome 24 sequence : 39

SRR10168389, number of contigs 3544
Clostridium baratii strain CDC51267 chromosome, complete genome : 57
Clostridium baratii str. Sullivan, complete genome : 51
Lutra lutra genome assembly, chromosome: 16 : 33
Staphylococcus aureus strain WH9628 chromosome : 29
Sus scrofa 18S ribosomal RNA gene, complete sequence : 27
Homo sapiens clone N29M24 sequence : 26
Homo sapiens clone LA14_101B3 sequence : 26
Mus musculus clone contig 1 chromocenter region genomic sequence : 25
Mouse DNA sequence from clone RP23-81C12 on chromosome 17, complete sequence :
25
Homo sapiens clone LA15_25H3 sequence : 24

SRR10168390, number of contigs 6993
Trypanosoma cruzi cruzi strain Sylvio X10/cl1 chromosome TcI7 sequence : 27
Oscheius tipulae isolate CEW1 chromosome V : 27
Lactobacillus gastricus strain LG045 chromosome, complete genome : 24
[Candida] glabrata strain BG2 chromosome M : 23
Lutra lutra genome assembly, chromosome: 16 : 22
Staphylococcus condimenti strain DSM 11674, complete genome : 20
Staphylococcus condimenti strain NCTC13827 genome assembly, chromosome: 1 : 20
Staphylococcus condimenti strain StO 2014-01, complete genome : 17
Lactobacillus mucosae LM1, complete genome : 17
Staphylococcus condimenti strain FDAARGOS_1148 chromosome, complete genome : 16

SRR10168391, number of contigs 10811
Myroides phaeus strain 18QD1AZ29W chromosome, complete genome : 337
Acinetobacter bereziniae strain GD0320 chromosome, complete genome : 168
Acinetobacter bereziniae strain GD03185 chromosome, complete genome : 148
Acinetobacter bereziniae strain XH901, complete genome : 145
Myroides odoratimimus strain G13 chromosome, complete genome : 117
Vagococcus carniphilus strain ATCC BAA-640 chromosome, complete genome : 112
Myroides sp. A21, complete genome : 100
Myroides odoratimimus strain PR63039, complete genome : 92
Beta vulgaris subsp. vulgaris cultivar KWS2320 chloroplast, complete genome :
91
Myroides sp. ZB35, complete genome : 86

SRR10168392, number of contigs 21005

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Lutra lutra genome assembly, chromosome: 16 :  107
Staphylococcus aureus strain WH9628 chromosome :  88
Sus scrofa 18S ribosomal RNA gene, complete sequence :  87
Mouse DNA sequence from clone RP23-81C12 on chromosome 17, complete sequence :
82
Homo sapiens clone LA14_101B3 sequence :  79
Homo sapiens clone N29M24 sequence :  77
Homo sapiens clone LA15_25H3 sequence :  77
Mus musculus clone contig 1 chromocenter region genomic sequence :  76
Homo sapiens clone LA13_165F6 sequence :  75
Human DNA sequence from clone bP-2171C21 on chromosome 21, complete sequence :
74


SRR10168393, number of contigs 10877
Homo sapiens DNA, chromosome 16, nearly complete genome :  221
Eukaryotic synthetic construct chromosome 16 :  213
Homo sapiens 16p13.3 sequence section 1 of 8 :  98
Homo sapiens interleukin 9 receptor (IL9Rps) pseudogene, complete sequence; and
DNA-directed RNA polymerases III 12.5 kDa polypeptide (POLR3K), U11/U12 snRNP 25
kDa protein (C16orf33), RHBDG1 (C16orf8), DNA-3-methyladenine glycosylase (MPG),
-14 gene protein (C16orf35), hemoglobin zeta subunit (HBZ), HBD (HBD), alpha
globin (HBA2), alpha globin (HBA1), theta globin (HBQ1), and putative RNA-
binding protein Luc7-like 1 (LUC7L) genes, complete cds :  96
Homo sapiens 16p13.3 sequence section 2 of 8 :  67
Homo sapiens chromosome 11, clone CTD-2643I7, complete sequence :  66
Eukaryotic synthetic construct chromosome 19 :  50
Eukaryotic synthetic construct chromosome 17 :  47
Homo sapiens DNA, chromosome 17, nearly complete genome :  46
Homo sapiens DNA, chromosome 19, nearly complete genome :  44
```

[57]:
```
### Get specific contigs matching a species/name
```

[58]:
```
def write_contigs(sra, match_names):
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    asc_matches=[]
    for m in match_names:
        for a,d in zip(accessions, descriptions):
            if m.lower() in d.lower():
                asc_matches.append(a)
    gi_matches=[]
    for a in asc_matches:
        idx=ACCESSIONS.index(a)
        gi=GIS[idx]
        gi_matches.append(gi)
```

```
    contigs=[]
    path = BASE_PATH+sra+'/magic_blast/'
    subset_f = open(path+f'{sra}_{match_names[0].replace(" ",␣
↪"_")}_subset_{f_contigs_file_tail}', 'w')
    with open(path+f'{sra}{f_contigs_file_tail}', 'r') as f:
        lines = [line for line in f]
        for line in lines:
            for gi in gi_matches:
                if gi in line:
                    parts=line.split('\t')
                    idx=GIS.index(gi)
                    asc=ACCESSIONS[idx]
                    t=TITLES[idx]
                    ps=parts[:2]
                    pe=parts[3:]
                    ps.append(asc+' '+t.rstrip('\n'))
                    parts=ps+pe
                    p='\t'.join(parts)
                    subset_f.write(p)
    subset_f.close()
```

[ ]:

[59]:
```
#set_accessions()
#assert ACCESSIONS is not None
```

[60]:
```
#match_names=['vector']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

[61]:
```
#match_names=['plasmid']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

[62]:
```
#match_names=['mustela']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

[63]:
```
#match_names=['virus']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```